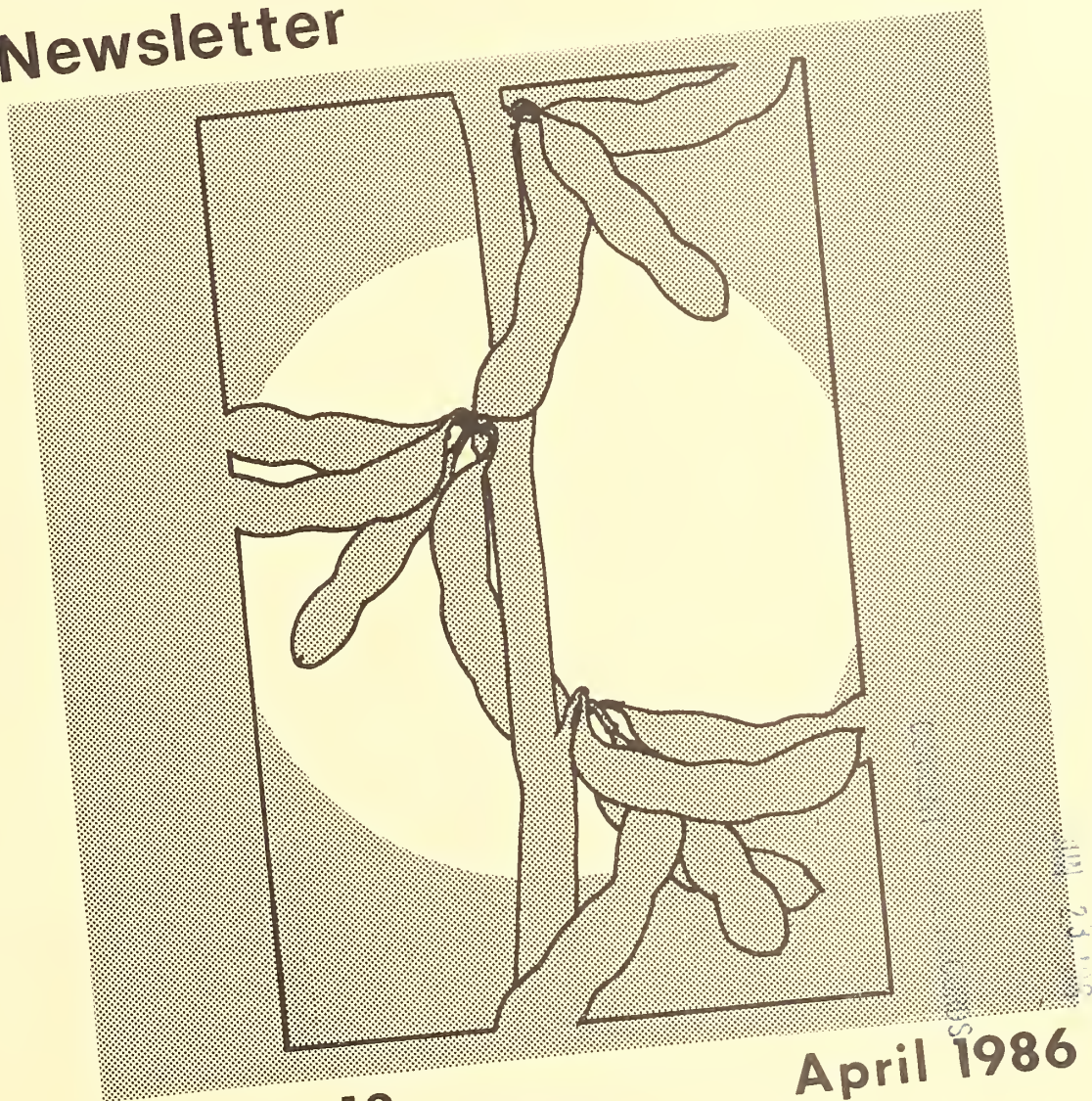


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Soybean Genetics Newsletter



Volume 13

April 1986

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publications without the consent of the respective authors.

Agricultural Research Service - USDA
Department of Agronomy
and Department of Genetics
Iowa State University
Ames, Iowa 50011

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I. FOREWORD

The mailing list of the Soybean Genetics Newsletter is printed for the convenience of soybean scientists wishing to contact other scientists in particular states or countries, or seeking addresses of scientists they know of but cannot locate. Volume 13 mailing list will reflect the three-year cyclical nature of this list: Each three years, subscribers are asked to reaffirm their wish to remain on the list by filling out and returning a coupon sent to them in the annual Request for Articles each October. And, of course, some coupons are lost, some are ignored, but most are returned. This issue's list will be shorter than usual, because we retain on the list ONLY those returned. Then, through the succeeding three years, we get individual letters and notes requesting the back issue(s) and asking that the name be returned to the mailing list. Therefore, if you seek a soybean scientist's address that isn't in Volume 13, look in Volume 12; he or she just may have neglected to return the coupon.

Each year at this time we make, to ourselves, the promise that we will adhere more closely to the declared deadline of 1 February for receipt of articles for the newsletter. When the task of preparing the newsletter for publication runs into preparation for spring planting, we're all stressed. So, now again, we make to you the promise (or threat) that we MUST receive manuscripts by 1 February for them to be considered for publication in the *Soybean Genetics Newsletter*.

We receive many requests for back issues of the Newsletter, and we fill these requests as much as possible. Although we print a large number of newsletters beyond our mailing list, we have, over the years, run out of copies of Volumes 1, 2, 3, 4, 5, 9, and 11. Volumes 1, 2, and 3 were reprinted, through the kindness of Robert Judd of the National Soybean Crop Improvement Council, Keith Smith of the American Soybean Association Research Foundation, and John Pesek of the Department of Agronomy at Iowa State. Costs of printing have gone up and up over the years; mailing costs have risen phenomenally. So, this winter we sent out a call for help to private seed companies, agricultural chemical companies, and genetic research institutions. We are extremely grateful to Agracetus, Asgrow Seed Company, Calgene, Dow Chemical Company, Funk Seeds International, King Agro, Inc., Land O'Lakes Research, Lilly Research Laboratories, Monsanto Agricultural Company, Pioneer Hi-Bred International, Inc., Sungene Technologies Corp., United Agriseeds, Inc., and The Upjohn

Company for their financial assistance. We are also pleased, proud, and grateful that an individual scientist, Dr. Theodore Hymowitz, respected the *Soybean Genetics Newsletter* enough to make a sizeable contribution.

The monetary votes of confidence give us the encouragement (and dollars) so necessary if we are to continue publishing the *Newsletter*.

Volunteers who helped with Volume 13, in diverse tasks such as proofreading, reference research, and citation checking include graduate students, technicians and undergraduate parttime workers. They are: Pamela Arney, Anita Bries, Duane Garien, Brad Hedges, Holly Heer, and Rhonda Honeycutt.

*The data presented in the Soybean Genetics Newsletter
are not to be used in publications without the
consent of the respective authors.*

*Mention of a trademark or proprietary product
by the USDA or Iowa State University does not
imply its approval to the exclusion of other
products that may also be suitable.*

II. PREREGISTRATION INFORMATION FOR THE
 CONFERENCE ON MOLECULAR AND CELLULAR BIOLOGY OF THE SOYBEAN
 29-31 July, 1986
 Iowa State University, Ames, Iowa U.S.A.

A program has been developed for participants in the Conference on Molecular and Cellular Biology of the Soybean that will provide an opportunity for formal and informal exchange of information. Formal presentations will include four plenary papers and contributed oral and poster papers. In addition, there will be ample opportunity for persons to discuss ideas informally.

Conference Program: The four plenary speakers were chosen to present the most current information on important aspects of plant molecular and cellular biology.

Dr. Alan Darvill, Complex Carbohydrate Research Center, University of Georgia

Title: Oligosaccharins, a new class of regulatory molecules in plants

Dr. W. A. Keller, Ottawa Research Station, Agriculture Canada

Title: Development of cell culture technology for the genetic manipulation of *Brassica* crops

Dr. Brian Larkins, Department of Botany and Plant Pathology, Purdue University

Title: Transformation and gene expression

Dr. Carolyn Napoli, Department of Plant Pathology, University of California-Berkeley

Title: Molecular genetics of host-pathogen interactions

The remainder of the papers at the conference will be contributed by the participants. Contributed papers will be presented orally or as a poster in English. The preference of the authors for the type of presentation will be respected as much as possible. To facilitate scheduling, the program committee may find it necessary to ask some authors to change their type of presentation.

Specific topics to be discussed in the conference include:

- Host-plant interaction
- Nitrogen fixation
- Molecular aspects of genetic diversity
- Plant regeneration
- Selection at the cellular level
- Gene transfer
- Protein and oil synthesis

Preliminary Program Schedule

Tuesday, 29 July

1000	Registration and poster set up
1300	Plenary paper, Dr. Carolyn Napoli
1430	Oral contributed papers
1830	Barbecue dinner and reception

Wednesday, 30 July

0900	Plenary paper, Dr. W. A. Keller
1030	Oral contributed papers
1330	Oral contributed papers
1500	Poster session
2000	Plenary paper, Dr. Brian Larkins

Thursday, 31 July

0900	Plenary paper, Dr. Alan Darvill
1030	Oral contributed papers
1200	End of conference

Welcome to Iowa State University and Ames: Iowa State University, the host for the Conference on Molecular and Cellular Biology of the Soybean, is a land-grant institution with an enrollment of more than 25,000 students. The conference will be held in the Iowa State Center, a multipurpose complex. The Scheman Continuing Education Building will serve as the meeting area.

Ames is a community of about 45,000 residents located 35 miles north of the state capital, Des Moines. The weather in Ames during July will be warm and humid. The daily low temperature averages 16°C and the daily high averages 29°C. All meeting facilities will be air-conditioned.

Registration: We have enclosed forms for preregistration and for the reservation of housing and food service. Early receipt of the forms will permit us to serve you best. The cost for registration will increase by \$10 after 15 May.

The registration fee includes one copy of the abstracts of papers to be presented at the conference. There will not be a proceedings. Registration packets will be available at the Scheman Continuing Education Building beginning at 1000 on Tuesday, 29 July.

Lodging: Lodging will be available in the university residence halls and at motels in the city. All persons who want to reserve space in the residence halls are asked to complete the Housing and Food Service Form. Persons who do not desire to reside in the residence hall are asked to make their own motel reservations with the information provided.

Campus Housing: Air-conditioned rooms will be available in the Maple-Willow-Larch Residence Hall complex across the street from the Iowa State Center. The excellent location and modest cost will make it an attractive choice for conference participants. Each room has two twin-size beds, two desks with chairs, a large chest of drawers, and ample closet space. One bathroom for women and another for men are located on each floor. A blanket, pillow, bed and bath linens, individual bath soap, and a drinking glass are provided for each person. Towels and washcloths are exchanged daily. The rooms will accommodate up to two adults and two children. Cots will be available for children in the same room as an adult at the rate of \$5 per night. Adjacent rooms will be provided to families upon request.

Room check-in will be held on the main floor of the Maple-Willow-Larch Residence Hall. The rooms can be occupied beginning on Monday, 28 July, and must be vacated by 1300 on Friday, 1 August. Your arrival time should be provided on the Housing Form to be certain someone is on duty at the time. Payment for lodging should be in U.S. dollars such as cash, personal check, or traveler's check. Credit cards are not accepted.

Motels: A listing of motels in the Ames area and their accommodations and telephone number is available. Their location relative to the Scheman building is indicated on the accompanying map. Motel residents will need to provide their own transportation to the Iowa State Center. City bus service serves some motel areas.

Food Service: Meal packages will be available in the residence halls for all conference participants. Well balanced meals are served cafeteria style in the dining room of the residence hall and correspond to the regular menus served to the students during the school year. Breakfast is served from 0630 to 0830, lunch from 1130 to 1300, and dinner from 1700 to 1830. It is important to indicate if you desire a meal package when you complete the Housing and Food Service Form. The meal package should be purchased at the housing desk of the residence hall complex when you arrive. Conference participants can purchase a meal package, even if they are not lodging in the residence halls.

Individual meals can be obtained at the Memorial Union of Iowa State University, located about four blocks from the Iowa State Center. It is a similar distance to various fast-food restaurants that serve an assortment of menus. More elaborate dining facilities are one to three miles from the Iowa State Center.

Continental breakfasts and a buffet lunch will be available each day at the Scheman Building. Individuals will be able to purchase the meals individually or can acquire a meal ticket.

A barbecue dinner and reception will be held on Tuesday, 29 July at the Scheman Building for conference participants and their families. The cost of the dinner/reception is \$10.00 per person. Please indicate the number of tickets desired on the preregistration form and include payment with the preregistration fees.

Travel Arrangements: Car: Ames is conveniently located on Interstate 35. Persons traveling by car will find ample free parking at the Iowa State Center and at all lodging facilities.

Bus: The Greyhound and Jefferson bus companies provide service to Ames. The downtown station is located about one mile from the Iowa State Center and residence hall complex. Passengers arriving by bus can use the local bus or taxi service.

Persons traveling by commercial airline will arrive at the Des Moines airport, about 40 miles south of Ames. There are a limited number of flights to Des Moines each day; therefore, we encourage you to make your reservations early.

Limited shuttle bus service is available between Ames and the Des Moines airport. We will arrange for extra bus service to serve conference participants, so it is important that you indicate your arrival and departure times on the Preregistration Form. We cannot guarantee transportation from the Des Moines airport to Ames for those persons who do not inform us by 15 July of their arrival time. Extra bus service also will be arranged for departures on Thursday when the morning session is completed. The cost for bus service will be \$10 one way, payable in cash when you arrive at the airport.

Special Needs/Disabilities: Please indicate on the Preregistration Form any special services you may need to accommodate handicaps or other situations.

CONFERENCE ON MOLECULAR AND CELLULAR BIOLOGY OF THE SOYBEAN
INFORMATION FOR ABSTRACT PREPARATION

1. This abstract must be prepared as a camera-ready copy for photoprinting. *No editorial corrections will be made.* Type the abstract on one sheet of 21.6 cm wide by 27.9 cm deep (8.5 x 11 inches) good quality, white bond paper using 3.8 cm (1.5 inch) margins on all sides. See the next page for a partial example.
2. Use an electric typewriter or letter quality printer with a black ribbon. Use black ink for adding symbols not on the typewriter. Do not try to make carbons at this typing. Erasures reproduce as smudges.
3. Start the title flush left. Capitalize all letters on the title. Titles should have at least 5 but not more than 10 words, and should contain keywords that identify the subject area.
4. Type the name of the author(s) on the line below the title, beginning 5 spaces in from the left margin. Capitalize only the initials and first letter of the last name of the author(s). An author's institution and address follows his or her name.
5. Leave one blank line between the last author-institution line and the text. Begin the text flush with the left margin. The abstract should be a brief, factual summary of the contents and conclusions of the paper. *Abstracts are limited to one page.* Text should be single-line spaced.
6. *Do not fold the abstract when mailing it.* In submitting the abstract, please provide the following information on a separate page: Title of paper, name of speaker, type of presentation preferred (oral or poster), and name, address, and telephone number of the corresponding author. In addition, indicate the general subject area of the paper, choosing from the list on page 3, if possible.
7. *The deadline for receipt of abstracts is 15 May 1986.* Mail abstracts to
Soybean Molecular and Cellular Biology
6 Agronomy
Iowa State University
Ames, Iowa 50011 USA

SEED PROTEIN ELECTROPHORESIS PROFILES OF WILD SOYBEAN (G. SOJA)
IN CHINA

B. Xu, S. W. Zhao, S. H. Zou, and H. Y. Zheng, Soybean
Institute, Gongzuling, PRC, and A. Z. Hu, Institute of
Botany, Beijing, PRC

Seed protein extracts from 178 collections of wild soybean (G. soja Sieb. & Zucc.) in China, originating from 24°-51° N, 97°-132°E, were analyzed by polyacrylamide gel electrophoresis to determine the geographical distribution of alleles of the Ti (Ti^a, Ti^b, Ti^c, ti) and Spl (Spl^a, Spl^b) loci

Information on Contributed Papers

Oral Papers:

1. Each paper will be 15 minutes in length, including time for discussion. Projectors for 5 x 5 cm slides, and overhead projectors, will be available.

Poster Papers:

1. The space available for each poster is 120 cm long by 120 cm high (4 ft by 4 ft). The posterboard, with a poster number in a 13 cm (5.1 inch) square in the upper left-hand corner, will be set up by the conference. The authors should attach the following information to the space remaining in the top 13 cm of the poster: the title of the paper, name of the authors, and the names of their institutions, as they are typed on the abstract form to be submitted for publication. The remainder of the space can be used for the text of the paper, which should include an abstract and a list of conclusions.
2. The title of the paper should be concise and readable from 4 m. The text should be readable from 1 to 2 m with letters 6 to 12 mm high.
3. Keep tables and charts simple. Use color when possible. Include legends and labels. Photographs with a matt finish are preferred over those with a glossy finish.

RESERVATION FOR HOUSING AND FOOD SERVICE IN THE ISU RESIDENCE HALLS

CONFERENCE ON MOLECULAR AND CELLULAR BIOLOGY OF THE SOYBEAN

29-31 July 1986

Housing Reservation

Please submit one copy of the form for each room desired. When two adults are sharing a room, only one application should be submitted. The confirmation of the reservation will be sent to the person whose address is provided.

Name _____ Telephone _____

Address _____ Arrival date and time _____

_____ Departure date and time _____

_____ Female _____ Male _____

Other adult occupant _____

Arrival date and time _____ Departure date and time _____

Accommodation preferred:

- ☐ Single (\$15/night)
☐ Double (\$10/person/night), person sharing the room is listed above.
☐ Double (\$10/person/night), conference will assign a roommate.
☐ Cot for child in room with parents (\$5/night), No. _____ (Maximum of two cots/room).

If adjacent rooms are required for children, please indicate the number of rooms needed _____. Do not submit a separate form for the adjacent rooms requested.

Ages and names of children in adjacent room(s) _____

Food Service Reservation

Meal packages in the Iowa State University Residence Hall are available for all conference participants. The \$12.25 package includes two breakfasts, (Wednesday and Thursday), one lunch (Wednesday) and one dinner (Wednesday).

Number of meal packages desired _____.

Names of persons requesting food service, if not listed above _____

The completed form should be sent to: Soybean Molecular and Cellular Biology, 6 Agronomy, Iowa State University, Ames, Iowa 50011 USA.

Telephone: 515/294-6865.

Do not pay in advance for lodging or meal packages in the ISU Residence Halls. Pay with cash, personal check, or traveler's check in U.S. dollars at the time of arrival. Credit cards are not accepted.

PREREGISTRATION FORM

CONFERENCE ON MOLECULAR AND CELLULAR BIOLOGY OF THE SOYBEAN
29-31 July 1986, Iowa State University, Ames, Iowa U.S.A.

This form must be received by 15 May 1986 to avoid charges for late registration. *Please type.*

Name _____
 Last *First* *Middle*

Name of company
or institution _____

Position/Title _____

Address _____

Telephone _____

Please note: Refunds of registration fees will be made if a written request is received by 22 July 1986. A \$5.00 processing fee will be assessed for all refunds.

Please indicate your preregistration status below.

By 15 May	After 15 May	
\$50.00 _____	\$60.00 _____	Full registration
\$25.00 _____	\$35.00 _____	Student registration

Barbecue tickets: No. _____ x \$10.00 = \$ _____.

Special accommodations needed for handicapped persons, etc. (explain) _____

For persons arriving by air, please indicate the following:

Arrival date _____ Time _____ Airline and flight number _____

Departure date _____ Time _____ Airline and flight number _____

Contact the address listed below if your arrival schedule changes from that indicated above.

Please mail above form with registration fees and payment for barbecue dinner ticket(s) to: Soybean Molecular and Cellular Biology, 6 Agronomy, Iowa State University, Ames, Iowa 50011 U.S.A. Telephone: 515/294-6865. Make checks payable to Iowa State University.

III. SOYA

Computerized Bibliographic Database on Soybean Utilization, Processing, Marketing, Nutrition, Production, and History

1100 B.C. to the Present

Background and Introduction: SOYA is the world's most comprehensive computerized bibliographic database relating to all aspects of soybeans and soyfoods. The *only* computerized database on foods with records predating the late 1960s, it contains more than 6,500 records published before 1969. Ten years in the making and international in scope, it is based on the Soyfoods Center Library, the world's largest in this field.

Producer and Owner of Database: Soyfoods Center, PO Box 234, Lafayette, CA 94549 USA. Phone: (415) 283-2991. Contact William Shurtleff. The Soyfoods Center is a private research and publication organization.

Subject Matter and Scope of Database: All aspects of soybean utilization and processing for food, feed, and industrial uses. Soyfoods include traditional and modern, fermented and nonfermented, soy oil, soybean flour and meal, and modern soy protein products. Marketing of soybeans and soyfoods worldwide, and information about these industries and markets. Nutrition and biochemistry of all foods and feeds. Major soy-related people and organizations. History of soybeans and soyfoods, domestication and dissemination of the soybean, history of world soybean production.

Of the tens of thousands of articles and books on all aspects of soybean agriculture (production, agronomy, etc.) that have been published worldwide, references to about 1,500 of the most important ones, including all key reviews of the literature, have been included in this database. Most of those published before 1925 have been included, as they are of historical importance.

Indexing/Coding/Classification: The bibliographic records (references) are indexed using one large index, which covers the following fields and allows virtually instantaneous retrieval: Personal Author, Corporate Author, Title in English, Journal Name, Keywords/Descriptors (controlled vocabulary), Corporate Source (authors' address), Language, and Identifiers (uncontrolled vocabulary).

The database uses 320+ Keywords, which are described in our Thesaurus (\$9.95). Each record contains at least one soy-related keyword plus a region-and-country keyword (e.g., Asia-Japan or Europe-France). Some records (such as major books) contain as many as 20 keywords.

Present Number of Bibliographic Records in Database: 10,900+ as of Jan. 1986.

Time Span Covered by Database: 1100 B.C. to present.

Principal Language of Database: English.

First Available in Machine-Readable Form: 10 December 1984.

Frequency of Updates: Monthly.

Growth Rate: 1,000 to 2,000 records/year.

Formats and Sequences Available: Format 1 is the full record. Format 2 is the bibliographic citation only (the first 15 fields, described later). The record sequence may be specified as either alphabetically by author, chronological, or reverse chronological (newest first).

Book Form: In 1986 (and roughly once every 3-5 years thereafter) the entire contents of the SOYA database will be printed as a hardcover book titled *Bibliography of Soyfoods and the Soybean Industry*. All records will be printed alphabetically by author and numbered sequentially. Then there will be a chronological listing of all records published before 1920. Finally, there will be a listing of all 320+ keywords, followed by the number of each record in which they occur. E.g., TOFU: 23, 99, 107, 108, 113, 176,

How to Search the Database: Contact The Soyfoods Center by phone (preferably) or letter, indicating subjects, authors, and/or time frame you wish to have searched. We will be glad to help you define your search. Online searching is not yet available. We will conduct the search immediately (using our indexes) and let you know the number of records found in each search, and the cost.

In any field relating to soybeans, the SOYA database is unsurpassed for doing a review of the literature. A sample request might be: "I'd like all references to soybeans or soyfoods in India from earliest times, printed alphabetically by author." Result: 227 references, starting from the year 1690.

Thesaurus for the SOYA Database, first published in 1985 and updated annually, is the key guide to searching. Containing all of the 320+ keywords, it shows hierarchical broad and narrow term relationships, related terms, and "see" references. It is available from Soyfoods Center for \$9.95, postpaid.

Prices: \$0.45 per record printed offline, \$45.00 minimum. Postpaid. Reduced rates for more than 500 records.

Full Text of Documents: Photocopies of the full text of most documents listed in the SOYA database can be ordered from Soyfoods Center Library for \$0.50 per page, \$9.00 minimum, postpaid. Orders must be prepaid.

How to Order: Orders must be prepaid until customer credit is established. Credit will automatically be given to staff members at all colleges and universities, and to well known organizations in the United States.

Hardware and Software: Our system uses two IBM-PCs, each with a hard disk (35 and 20 megabytes). Our database manager program, called BIBLIO, is based on Revelation. One of the world's most powerful bibliographic software programs, BIBLIO is available to organizations developing computerized bibliographic databases. For a detailed brochure and prices, contact the Soyfoods Center.

Number of Records and Composition of Database by Time Periods:

1100 B.C. to 1849	152 records	1.7% of total
1850 to 1900	405 records	4.5%
1900 to 1919	881 records	9.7%
1920 to 1939	1532 records	16.9%
1940 to 1959	1817 records	20.0%
1960 to 1968	1685 records	18.6%
1969 to 1985	3102 records	34.2%

Number of Records on Major Food Categories in Database:

1148	Soy oil and soybean meal
1107	Soy flour
806	Tofu
755	Soymilk
609	Soy sauce
655	Modern soy proteins (Isolates, concentrates, textured products)
484	Miso
473	Tempeh
201	Whole dry soybeans
199	Fresh green soybeans
191	Soy sprouts
176	Soy ice cream (from isolates, tofu, or soymilk)
162	Soy lecithin
161	Natto
117	Fermented soymilk products

Number of Records about Major Regions and Countries (Other than USA)

1742	Asia, East
	1057 Japan
	407 China (People's Republic)
	105 Manchuria (before 1949)
	76 Korea
1431	Europe
	370 Germany
	283 France
	263 United Kingdom
	96 USSR

379	Southeast Asia
	179 Indonesia
370	Latin America
	116 Brazil
308	Indian Subcontinent
	227 India
	53 Sri Lanka
193	Africa

Number of Records about Major Organizations in the Database:

585	Research Centers (USDA/NRRC, Cornell, Univ. of Illinois, INTSOY, etc.)
	312 Northern Regional Research Center
	128 Cornell University (Incl. Agric. Exp. Station in Geneva, N.Y.)
539	Soybean Crushers (ADM, Cargill, Central Soya, Staley, Ralston, etc.)
	113 Central Soya
403	Pioneer soybean states (Illinois, N. Carolina, Massachusetts, Kansas)
	159 Illinois (State and University)
	113 North Carolina
295	American Soybean Assoc.
218	U.S. Department of Agriculture (not incl. Agric. Experiment Stations)
216	Seventh-day Adventists
186	Pioneer soy protein manufacturers (I.F. Laucks, Glidden, Rich Products, Gunther Prods., Griffith Labs.)

Number of Records about Soybean Production and Trade:

1709	Total (not including individual states and organizations)
249	Soybean plant protection
	101 Pest control (mainly insects and nematodes)
	77 Disease control
	61 Weed control
198	Variety development and breeding
171	Trade of soybeans and soybean products
169	Soybean culture and management
105	Soybean marketing and economics
69	Nitrogen fixation, rhizobia

Number of Records on Other Major Categories

1026	Nutrition value of soyfoods
396	Industrial soy products

Number of Records and Composition of Database by Primary Language

5048	English	82.4%	55	Dutch	0.58%
537	Japanese	5.6%	55	Portuguese	0.58%
387	German	4.0%	52	Italian	0.55%
281	French	3.0%	33	Russian	0.35%
93	Spanish	0.98%	98	Other	1.04%
83	Chinese	0.87%		(Latin 26, Korean 24, Indonesian 19, Swedish 16, etc.)	

Number of Records and Composition of Database by Document Type:

6379	Journal articles, from over 780 journals worldwide*....	67.1%
916	Books	9.6%
588	Conference papers	6.2%
375	Patents	3.9%
262	Booklets	2.8%
192	Book chapters	2.0%
144	Reports	1.5%
95	Unpublished manuscripts	1.0%
87	Theses	0.91%
320	Other (Ads, serials, leaflets, conference proceedings, lectures, letters, films, abstracts, etc.	3.37%

*Includes magazine and newspaper articles, serial reports and bulletins.

Fields in Each Record:Part I: The Bibliographic Citation

Record Number (the key; unique for each record)
 Personal Author(s)
 Corporate Author(s)
 Author Notation (such as editor, translator)
 Year of Publication
 Title in English
 Title, Foreign (Non-English)
 Document Type (e.g., book, journal article)
 Journal Name or Patent Country Name
 Volume, Issue, Pages, or Patent Number
 Publication Data for Books or Theses
 Book or Thesis Pages
 Addenda (additional information of any type)
 Language(s)
 Number of References

Part II: Keywords and Additional Information

Keywords (up to 20 controlled terms per record)
 Holding Library and Call Number (Given for most hard-to-get documents)
 Corporate Source (Address of author(s))
 Country of Publication
 Additional Authors
 Cited by (like Science Citation Index)
 Questions (for in-house use only)
 Importance (scale of 1-10, used mainly for classics)
 Identifiers (uncontrolled terms)
 Notes

Comparison of SOYA and Other Soy Related Databases

Characteristic	SOYA	FSTA	AGRICOLA	EMBRAPA/ BIOSIS
Earliest record	1100 B.C.	1968	1970	1970
No. of Records before 1969	6,472	0	0	0
Strengths by Subject Matter	Utilization, Marketing, History	Food Science Technol.	Agriculture, Livestock	Agriculture, Livestock Biology
Total Soy-related Records as of Oct. 1985	10,000	7,287	19,920	20,000
Soybean Utilization and Nutrition Records	8,200	5,631	3,048	3,500
Non-Utilization, mostly Soybean Production	1,800	1,656	16,872	16,500
Records on Tofu	806	165	111	20
Soymilk	755	315	163	51
Tempeh	473	63	50	26
Soy flour	1,107	421	239	544
Soy sauce	709	596	224	109
Miso	484	403	64	31
Natto	161	45	28	16
Soy proteins	962	2,122	1,099	858
Soy oil	1,148	1,220	620	537
Total of Above 9 categories	6,605	5,262	2,598	2,192
Price: Online connect hour	0	\$63.00	\$35.00	\$66.00
Full rec. printed offline	\$0.45	\$0.15	\$0.10	\$0.28

*Development of this SOYA database was supported in part by generous grants in aid from the Hong Kong Soya Bean Products Co., Ltd. (makers of Vitasoy brand soy beverages) and from the Kikkoman Corporation.

KW = SoyaDesc.BIB Started 4/85. 2 Jan. 1986 revision

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Tel (415) 283-2991

IV. SOYBEAN GENETICS COMMITTEE REPORT

Minutes of the Meeting

The Soybean Genetics Committee met Monday, Feb. 24, 1986, at the Sheraton Inn, St. Louis, MO. This meeting was held in conjunction with the annual Soybean Breeders Workshop.

Committee members in attendance were W. D. Beversdorf, R. L. Bernard, H. R. Boerma, X. Delannay, T. E. Devine, R. I. Buzzell, J. R. Wilcox, and R. G. Palmer. Also present was T. Hymowitz. J. H. Orf and Y. T. Kiang have been elected to new three-year terms on the Committee, replacing H. R. Boerma and T. E. Devine, whose terms expired at the close of the meeting. Present committee members and the expiration of their terms are as follows:

R. L. Bernard, Ex officio
(Curator of soybean genetics
collection)

Department of Agronomy
University of Illinois
1102 S. Goodwin St.
Urbana, IL 61801

W. D. Beversdorf, Chairman (1987)
Crop Science Department
University of Guelph
Guelph, Ontario
Canada N1G 2W1

R. I. Buzzell (1988)
Agriculture Canada, Research Station
Harrow, Ontario
Canada NOR 1G0

X. Delannay (1988)
Monsanto Agricultural Company
St. Louis, MO 63198

Y. T. Kiang (1989)
Department of Plant Sciences and
Genetics
University of New Hampshire
Durham, NH 03824

J. H. Orf (1989)
Department of Agronomy and Plant
Genetics
University of Minnesota
St. Paul, MN 55101

R. G. Palmer, Ex officio
(Editor of Soybean Genetics Newsletter)
Departments of Agronomy and Genetics
Iowa State University
Ames, IA 50011

J. R. Wilcox (1987)
Department of Agronomy
Purdue University
West Lafayette, IN 47907

Dr. W. D. Beversdorf was re-elected chairman of the Committee for 1986. Manuscripts concerning qualitative genetic interpretation and gene symbols should be sent to him for review.

A few changes in the rules for genetic symbols were approved by the Committee. The changes in the gene symbol rules approved by the Committee are underlined in the rules published this year.

The Committee discussed the type and amount of data needed for the assignment of gene symbols. These guidelines are published in this Soybean Genetics Newsletter so those researchers submitting articles with the

assignment of new gene symbols will know what data are expected before the Committee will consider assigning a gene symbol.

A committee consisting of W. Beversdorf, X. Delannay and T. Hymowitz presented their report on the rules for gene symbols introduced into soybeans from other organisms via such methods as gene transfer, transformation and other genetic engineering techniques and also to consider rules for assigning gene symbols to genes in the perennial species of the subgenus *Glycine*. After considerable discussion, the Committee recommended that a revised report be prepared and presented at the 1987 Committee meeting.

The Committee urges researchers who report lines carrying new genes to submit a seed sample to Dr. R. L. Bernard so a genetic type collection designation (T-number) can be assigned. Dr. Bernard will maintain the seed and have it available on request.

Guidelines on the Evidence Necessary for the Assignment
of Gene Symbols

The following is a set of guidelines prepared by the Soybean Genetics Committee and intended to help researchers undertaking genetic analysis of soybean traits. Of necessity, these procedures will often need to be modified by the researcher to fit the specific situation, but an application of these guidelines should aid in making the correct genetic interpretation.

1. A genetic hypothesis is made on the basis of classification of segregating progeny, usually the F_2 generation and here called the hypothesis generation.
2. A second generation is classified to confirm the proposed genetic hypothesis. This second generation may be progeny of the hypothesis generation (usually F_3) or progeny of a testcross (F_1 x recessive homozygote).
3. Traits that are strongly influenced by nongenetic factors require verification of the classification scheme by evaluation of the progeny from homozygous plants of the hypothesis generation. Testcross data are not suitable for this purpose.
4. For genes controlling a phenotypic expression similar to that of previously published genes, data must be obtained to test for uniqueness and allelism. This will usually require crossing a homozygous line carrying the newly identified gene with the original sources of the previously published genes.
5. Follow the guidelines (Rules for Genetic Symbols) published in the Soybean Genetics Newsletter to assign the symbol.
6. Submit the manuscript to the chair, Soybean Genetics Committee, for review of the genetic interpretation and approval of the gene symbol (see Soybean Genetics Newsletter for name and address).
7. If the line in which the new gene occurs is not already in the USDA Germplasm Collection, send a seed sample of the line to the curator of the Genetic Type Collection for assignment of a T-number and maintenance of the seed (see current Soybean Genetics Newsletter for name and address).

References

- Mather, K. 1951. The measurement of linkage in heredity. Methuen & Co. Ltd., London. John Wiley & Sons, Inc., New York.

- Hanson, W. D. 1959. Minimum family size for the planning of genetic experiments. *Agron. J.* 51:711-715.
- Sedcole, J. R. 1977. Number of plants necessary to recover a trait. *Crop Sci.* 17:667-668.

Rules for Genetic Symbols

I) Gene Symbols

- a) Gene symbols should not be assigned to traits for which no inheritance data are presented.
- b) A gene symbol shall consist of a base of one to three letters, to which may be appended subscripts and/or superscripts as described below. Gene symbols may, however, be written on one line.
- c) Genes that are allelic shall be symbolized with the same base letter(s) so that each gene locus will be designated by a characteristic symbol base.
- d) Gene pairs with the same or similar effects (including duplicate, complementary or polymeric genes) should be designated with the same letter base differentiated by numerical subscripts, assigning 1, 2, 3, 4, etc., consecutively in the order of publication. (Example: Y_1 , Y_2 , etc.) The numerals may be written on the same line as the base. (Example: Y_1 , Y_2 , etc.) This shall be the only use of numerals. Letter designations should not be used. The numeral 1 is automatically a part of the first reported gene symbol for each base but may be omitted only until the second symbol is assigned.
- e) The first pair of alleles reported for a gene locus shall be differentiated by capitalizing the first letter of the symbol for the dominant or partially dominant allele. (Example: Ab , ab . Ab is allelic and dominant to ab .)
- f) If two alleles are equivalent, codominant, or if dominance is not consistent, the capitalized symbol may be assigned at the author's discretion and the alleles may be differentiated by adding one or two uncapitalized letters as superscripts to the base. When more than two alleles exist for a locus, the additional alleles or those symbolized subsequently to the pair first published shall be differentiated by adding one or two uncapitalized letters as a superscript to the base. (Example: R , r^m , r .) This shall be the only use of superscripts. The letters may be written on the same line as the base if preceded

by a hyphen. (For example, Rps1-b, Rps1-k, and Ap-a, Ap-b, Ap-c.) The base for the additional alleles is capitalized only when the gene is dominant or equivalent to the allele originally designated with a capitalized symbol. The letters may be an abbreviation of a descriptive term.

If independent mutations with the same or similar phenotypes are identified at the same locus, until it is possible genetically to ascertain if they represent identical or separate alleles, the gene symbol should be followed by an identifying designation preceded by a hyphen. The identifying designation, which should not be in italic or underlined, can be the place where the mutation was found, the cultivar in which it was found, or any other relevant characteristic of the mutation. (Example: *msl* -Urbana, *msl*-Tonica.) This will ensure that possible subtle differences between the mutations, such as differences in DNA sequence, or unique pleiotropic side effect, are not overlooked by workers using those genes.

- g) Base letters may be chosen so as to indicate apparent relationships among traits by using common initial letters for all loci in a related group of traits. Examples are P for pubescence type, R for disease reaction (plus two initials of the pathogen to complete the base), and L for leaf shape.
- h) The distinction between traits that are to be symbolized with identical, similar, or with unrelated base letters is necessarily not clear-cut. The decision for intermediate cases is at the discretion of the author, but should be in accordance with previous practices for the particular type of trait.

The following sections concern supplementary symbols that may be used whenever desired as aids to presentation of genetic formulas.

- i) An underscore may be used in place of a gene symbol to represent any allele at the indicated locus. The locus represented should be apparent from its position in the formula. (Example: A_ represents both AA and Aa.)
- j) A question mark may be used in place of a symbol when the gene is unknown or doubtful, or it may be used as a superscript or on the base line if preceded by a hyphen. (Example, a[?] or a-? indicates that the letter is an unknown allele at the A locus.)

- k) Plus symbols may be used in place of the assigned gene symbols of a designated standard homozygous strain when this will facilitate presenting genetic formulas. The standard strain may be any strain selected by the worker, as long as the strain being used and its genetic formula are made explicit.

II) Isoenzyme Symbols and Protein Gene Symbols

The following set of guidelines is to be used when assigning gene symbols to isoenzyme variants. As far as possible, these recommendations are consistent with the existing guidelines for assigning gene symbols in soybeans.

- a) A gene symbol (generally three letters) that indicates, as clearly as possible, the name of the enzyme should be used. The example, Adh (alcohol dehydrogenase); Idh (isocitrate dehydrogenase). The appropriate Enzyme Commission name and number should be used in the original article, when appropriate, to designate the specific enzyme activity being investigated.
- b) The electrophoretic conditions used to characterize a locus or allele should be specified clearly and in sufficient detail to be repeated by others interested in using the locus in genetic studies. The electrophoretic mobility, or other properties of an allele, should be clearly described by the authors.
- c) Publications should include a photograph and/or an interpretive zymogram that allows readers to visualize the variability described by the authors, as well as to ensure that subsequent work corresponds to the original study.

III) Linkage and Chromosome Symbols

- a) Linkage groups and the corresponding chromosomes shall be designated with arabic numerals. Linkage shall be indicated in a genetic formula by preceding the linked genes with the linkage group number and listing the gene symbols in the order that they occur on the chromosome.
- b) Permanent symbols for chromosomal aberrations shall include a symbol denoting the type of aberration plus the chromosome number(s) involved. Specific aberrations involving the same chromosome(s) shall be differentiated by a letter as follows: The symbol Tran shall denote

translocations. Tran 1-2a would represent the first case of reciprocal translocations between chromosomes 1 and 2, Tran 1-2b the second, etc. The symbol Def shall denote deficiencies, Inv inversions, and Tri primary trisomics. The first published deficiency in chromosome 1 shall be symbolized as Def 1a, the second as Def 1b, etc. The first published inversion in chromosome 1 shall be designated with the arabic numeral that corresponds to its respective linkage group number.

- c) Temporary symbols for chromosomal aberrations are necessary, as it may be many years before they are located on their respective chromosomes. Tran 1 would represent the first case of a published reciprocal translocation; Tran 2, the second case, etc. The first published deficiency shall be symbolized as Def A, the second as Def B, etc. The first published inversion shall be symbolized as Inv A, and the second as Inv B, etc. The first published trisomic shall be designated as Tri A, the second as Tri B, etc. When appropriate genetic and/or cytological evidence is available, the temporary symbols should be replaced with permanent symbols, with the approval of the Soybean Genetics Committee.

IV) Cytoplasmic Factor Symbols

- a) Cytoplasmic factors shall be designated with one or more letters prefixed by cyt-. (Example: cyt-G indicates the cytoplasmic factor for maternal green cotyledons, cyt-Y indicates that for maternal yellow cotyledons.)

V) Priority and Validity of Symbols

- a) A symbol shall be considered valid only when published in a recognized scientific journal, or when reported in the Soybean Genetics Newsletter, with conclusions adequately supported by data which establish the existence of the entity being symbolized. Publication should include an adequate description of the phenotype in biological terminology, including quantitative measurements wherever pertinent.
- b) In cases where different symbols have been assigned to the same factor, the symbol first published should be the accepted symbol, unless the original interpretation is shown to be incorrect, the symbol is not in accordance with these rules, or additional evidence shows that a change is necessary.

VI) Rule Changes

- a) These rules may be revised or amended by a majority vote of the Soybean Genetics Committee.

It is recommended that all gene symbols and genetic interpretation be reviewed by the Soybean Genetics Committee prior to publication to avoid duplication and/or confusion.

V. CROP ADVISORY COMMITTEES

The function of Crop Advisory Committees is to serve their crop commodity groups and provide expert advice to individuals or organizations, such as the National Plant Genetics Resources Board, the National Plant Germplasm Committee, the Agricultural Research Service, State Agricultural Experiment Stations, and others on technical matters relating to plant germplasm, its breeding, and effective utilization.

Duties and responsibilities:

1. Develop and provide a strategic overview of the total national scientific efforts in the study of and utilization of germplasm of specific crops or group of crops and recommend cooperative approaches for improvements in the germplasm management system where needs are apparent.
2. Assess the adequacy of the germplasm base for a specified crop or group of crops and make recommendations to appropriate governmental and private agencies for broadening and strengthening each base via additional exploration, collection, acquisition of private collections, and evaluation.
3. Assess progress in each crop through breeding and the role germplasm resources might play in improving traits of economic importance.
4. Suggest guidelines for the effective regeneration, increase, distribution, evaluation, and utilization of plant introductions and other accessions in each crop or group of crops.
5. Consider needs for fundamental and applied studies on each crop and make suggestions on promising research approaches and enhancement opportunities.
6. Assess the impact of biotechnology and genetic engineering on germplasm resource needs and utilization in their respective crops.
7. Monitor staffing and support requirements for research efforts relating to plant germplasm activities on individual crops, or groups of crops, and provide suggestions for training, staffing, and support needs.
8. Develop a better understanding of international germplasm activities on the crop(s) in question, identifying and describing implications for science and agriculture in the United States or in those institutions abroad that receive major support from this country.
9. Provide means for commodity groups to voice opinions on need for plant

germplasm resources, their improvement and utilization to those individuals responsible for these areas at the national level.

10. Assist variety review boards with respect to new variety developments and breeding progress in their respective crops.
11. Encourage the development and utilization of newsletters and/or reports giving a description of germplasm available for their crops.
12. Develop concise reports when requested by the NPGRB or the NPGC on on-going germplasm activities, resource needs, and action plans for each crop or group of crops.

VI. SOYBEAN GERMPLASM CROP ADVISORY COMMITTEE REPORT

The Soybean Germplasm Crop Advisory Committee held its annual meeting Feb. 24, 1986, at the Soybean Breeders' Workshop in St. Louis, MO. Twelve of the 14 members were in attendance. Also attending was Mark A. Bohning, Crop Advisory Committee Facilitator, Plant Genetics and Germplasm Institute. Those elected to three-year terms were: T. Scott Abney, USDA, Purdue University; J. Grover Shannon, Asgrow Seed Company; and Richard Wilson, USDA, North Carolina State University.

Updates on both the northern and southern portions of the USDA Soybean Germplasm Collection were given by Richard Bernard and Calton Edwards, respectively. Those reports are presented in the Soybean Genetics Newsletter, pages 42-46.

A report was given by a subcommittee (Richard Bernard, Reid Palmer, and Curtis Williams) on the perennial *Glycine* collections. The subcommittee recommended that all available perennial *Glycine* accessions be obtained and preserved in the U.S. Additional recommendations were that funding be provided to expand facilities and personnel at Urbana to handle the maintenance and distribution of the perennial *Glycine* species. The entire committee voted unanimously to support the recommendations of the subcommittee.

The Bylaws of the Committee were reviewed. Suggestions were made to date the bylaws and to publish them in the Soybean Genetics Newsletter (Vol. 13, pp. 31-32).

Curator activity needs were reviewed. Richard Bernard reported that repair was needed on the Urbana cold storage facilities to correct a leakage problem. He also proposed that curators take only written requests for germplasm, because of the time involved in taking a telephone request. Edgar Hartwig reported that Maturity Group X accessions were being grown in Puerto Rico.

Richard Bernard reported on the status of the International Board for Plant Genetic Resources (IBPGR) directory of world soybean collections and the Soybean Germplasm Collection Inventory. The IBPGR directory will be an INTSOY publication and is expected to be published before the end of 1986. The Soybean Germplasm Collection Inventory should be finalized by May, 1986. It also will be an INTSOY publication and will be released after the IBPGR directory.

Randall Nelson reported on the status of the germplasm evaluation publications. A preliminary report of the most recent evaluation of new accessions is now available. A final report will be published in 1987.

Current recommendations for soybean germplasm acquisition, maintenance, evaluation, and enhancement were reviewed. A discussion took place concerning the time and effort involved to keep our own varieties from being reintroduced into our collection. There was also a discussion of maintenance procedures and coordinated enhancement projects.

The FY 85 soybean germplasm enhancement and evaluation proposals were discussed. Mark Bohning suggested that the committee may wish to review these proposals, update if necessary, and resubmit as a means for identifying needs. The vice-chairman was appointed as head of a subcommittee to identify high priority needs on an annual basis in the areas of acquisition, maintenance, evaluation, and enhancement. A report of the subcommittee's recommendation will be submitted to members of the advisory committee prior to its annual meeting. After approval, recommendations will be submitted to the Chairman, National Plant Germplasm Committee.

Richard Bernard proposed a change in the name of our committee from Soybean Germplasm Advisory Committee to Soybean Germplasm Crop Advisory Committee. The change was adopted.

Mark Bohning reviewed the purpose of crop advisory committees (CAC), including parameters of duties and responsibilities. The chairman was directed to submit to the Soybean Genetics Newsletter the CAC Duties and Responsibilities. Beginning in 1987, the chairman is to send a list of the duties and responsibilities to committee members for potential revision each year.

Following are the current committee members, addresses, areas of representation, and dates of expiration of current terms:

Name	Address	Area of representation	Expiration of term
T. Scott Abney	USDA, ARS Dept. of Plant Pathology Purdue University W. Lafayette, IN 47907	Plant pathology	1989
R. L. Bernard	USDA, ARS Dept. of Agronomy University of Illinois 1102 South Goodwin Urbana, IL 61801	USDA germplasm collection	ex officio

Name	Address	Area of representation	Expiration of term
Edgar E. Hartwig	USDA, ARS Soybean Prod. Research P.O. Box 196 Stoneville, MS 38776	USDA germplasm collection	ex officio
Kuell Hinson	USDA, ARS Dept. of Agronomy University of Florida 304 Newell Hall Gainesville, FL 32611	Public breeding, south	1987
Clark Jennings	Pioneer Hi-Bred Int'l 3261 W. Airline Hwy. Waterloo, IA 50703	Private breeding, north	1987
Thomas C. Kilen	USDA, ARS Soybean Prod. Research P.O. Box 196 Stoneville, MS 38776	USDA germplasm collection	ex officio
R. A Kinloch	Agric. Research Center Route 3, Box 575 Jay, FL 32565	Nematology	1987
Phillip Miller	USDA, ARS Beltsville Agric. Res. Center Building 005, BARC-W Beltsville, MD 20705	USDA National Program Staff	ex officio
Randall Nelson	USDA, ARS Dept. of Agronomy University of Illinois 1102 South Goodwin Urbana, IL 61801	USDA germplasm collection	ex officio
J. H. Orf	Dept. of Agronomy and Plant Genetics University of Minnesota St. Paul, MN 55101	Plant breeding, north	1988
Reid G. Palmer	USDA, ARS 4 Curtiss Hall Iowa State University Ames, IA 50011	Cytogenetics and molecular genetics	1988
J. Grover Shannon	Asgrow Seed Company P.O. Box 210 Marion, AR 72364	Private breeding, south	1989

Name	Address	Area of representation	Expiration of term
M. J. Sullivan	Edisto Experiment Stn. P.O. Box 247 Blackville, SC 29817	Entomology	1988
Richard Wilson	414 Williams Hall N. Carolina State Univ. Raleigh, NC 27695-7620	Physiology	1989

Thomas Kilen was reelected as chairman of the committee and Clark Jennings was reelected vice-chairman. Both will serve one-year terms.

Thomas C. Kilen
Chairman
Soybean Germplasm Crop
Advisory Committee

VII. SOYBEAN GERMPLASM CROP ADVISORY COMMITTEE BYLAWS

FEBRUARY 1984 (adopted)

Membership: The Soybean Germplasm Advisory Committee will consist of 14 members. The curators of the northern and southern portion of the collection, the research geneticists working with the germplasm collection at each location, and a representative from the National Program Staff will serve as *ex officio* members. All *ex officio* members will have full voting privileges and may hold committee offices.

The remaining nine committee members will be elected to the committee to represent various geographical and/or research areas as follows:

1. Private breeder, north
2. Private breeder, south
3. Public breeder, north
4. Public breeder, south
5. Pathologist or nematologist
6. Pathologist or nematologist
7. Entomologist
8. Physiologist or biochemist
9. Cytogeneticist or molecular geneticist

Terms of office: Committee members will be elected to three-year terms and may serve no more than two consecutive terms. After an absence of at least one year from the committee, a former two-term member is eligible for membership again. Terms will begin following the annual meeting held in conjunction with the Soybean Breeders' Workshop in late February.

Committee officers: The committee shall have two elected officers, chairperson and vice-chairperson. Each officer will be elected to a one-year term at the committee's annual meeting to serve the following year and may serve no more than five consecutive terms. After an absence of at least three years from the office, a former five-term officer is eligible for re-election to that post.

The duties of the committee chairperson include coordinating annual elections, notifying members of meetings, chairing meetings, and other duties as necessary to fulfill the committee's responsibilities. The vice-chairperson shall record the proceedings of all meetings and assist the chairperson as requested.

Elections: Each year, three members will be elected in the following manner:

- Year 1: Entomologist
 Northern breeder, public
 Cytogeneticist or molecular geneticist
- Year 2: Southern breeder, private
 Physiologist
 Pathologist or nematologist (position A)
- Year 3: Northern breeder, private
 Southern breeder, public
 Pathologist or nematologist (position B)

By November 1 of each year, the chairperson will send a request for nominations for each position for which the incumbent's term expires the following February. These requests will be sent to those whose discipline and geographical areas are the same as the qualifications for the open committee position. All nominations must be received by the chairperson by November 30. If more than two nominations are received for any position, the chairperson will send all nominations to the committee and each member may vote for two candidates for each position. The ballots from this primary election must be sent by December 7 and returned to the chairperson by January 7. A final ballot with the top two candidates for each position will be sent to the committee by January 10. These ballots must be returned to the chairperson by January 27. The chairperson will then notify the newly elected members so that they may attend the annual meeting in late February. The newly elected members will officially begin their terms after that meeting but will be invited to attend as observers.

Rule changes: These rules may be amended by a majority vote (8) of the committee members.

VIII. COMMERCIAL SOYBEAN BREEDERS BOARD -- 1986

Curtis Williams - Chairman
Jacob Hartz Seed Co.
Box 946
Stuttgart, AR 72160
(501) 673-8565

Nancy Sebern - Vice Chairman
DeKalb-Pfizer Genetics
Beaman, IA 50609
(515) 366-2606

Alan Walker - Secretary
Asgrow Seed Co.
206 W. 11th Street
Redwood Falls, MN 56283
(507) 637-3011

Jimmy Barber
Funk Seeds International
Rt. 1, Box 540A
Greenville, MS 38701
(601) 335-4132

Roger McBroom
Northrup King Co.
306 Meadow Drive, Box Z
St. Joseph, IL 61873
(217) 479-2746

Thomas J. Wofford
Delta & Pine Land Co.
P.O. Box 1118
Wilson, NC 27893
(919) 237-8528

IX. A SUMMARY OF GENES FROM SOYBEAN MOLECULAR GENETIC STUDIES, 1978-1985

R. I. Buzzell

Agriculture Canada, Research Station, Harrow, Ontario

Considerable information has been published on the molecular genetics of soybeans in the past five years. Summaries are given for nuclear genes in Table 1, chloroplast genes in Table 2, and mitochondria genes in Table 3. In a few cases, genes known from classical studies have been researched by molecular analysis (17, 24, 50).

In contrast to classical genetics in which genes are identified from allelic segregation at a locus, techniques of molecular genetics use DNA sequences in identifying genes. Single copy DNA and repeated sequences become considerations with about 40% of the soybean nuclear genome being single copy and about 60% being repetitive sequences organized primarily with long regularly repeating tandem or clustered arrays (13, 36). Gene linkages are expressed in terms of nucleotide base pairs and the size of restriction enzyme fragments; for example, see Bojsen et al. (5). Somatic cell genetics also may be used.

Table 1. Soybean nuclear genes

Actin protein:	Small multigene family (19, 31, 33); pSac3 gene (48); SAcl gene (49).
Allantoin utilization as sole N:	Allantoin genes not linked to genes for asparagine dependence (40).
Beta-conglycinin (7S) seed protein:	Alpha and alpha' subunit multigene families (45, 46); alpha' subunit gene (2, 3, 47); deletion in most of the coding sequences in Cgyl (alpha' subunit) results in cgyl (24); 3 clones each with 2 genes (15).
Embryo mRNA:	Al6, A28, A36, A37 genes (16).
15 kd protein:	2 nonallelic genes (10); 15 kd1, 15 kd2 (14, 15).
Glycinin seed protein:	3 nonallelic genes G1, G2, G3 (10, 14, 15); A2B1a subunit gene (29); Ala subunit DNA (34); group II A3B4 and A5A4B3 subunit genes (41).
Heat shock proteins:	hs genes (42, 43); hs 6871, hs 6834 (44).
Kunitz trypsin inhibitor:	KTI genes (20); two genes separated by about 1 kb (15).
Leaf protein:	nonseed protein genes (10, 15).

Table 1. Continued

Lectin:	L1, L2 genes (17, 39); Le = L1 and le = L1 + 3.4 kb insertion (17, 39); L1, L2, SL (15).
Leghaemoglobin:	Lb genes 40 copies (1); Lb gene (22); six Lb genes (5, 7); normal, pseudo and truncated Lb genes (6); Lb genes LbT1, LbT2 (7); Lba, Lbc genes (21); Lba, Lbc, Lb ψ , Lbc3 and other Lb genes (25a, 25b, 28); Lb genes (26, 27, 55, 57, 59, 60, 61); LbC3 gene (30); Lbc-2 and Lbc-3 (64).
Meso-diaminopimelate dehydrogenase:	gene (63).
Non-Lb:	genes linked with Lb genes (5).
Nodulin (nodule protein):	Low copy NodA, NodB, NodC and NodD low copy gene sequences (12); nodulin-23 gene (30); nodulin-24 gene (23, 30); nodulin genes (58, 59, 60, 61).
Ribosomal RNA:	17S and 25S genes linked and tandemly repeated (56); 18S and 25S tandemly repeated multigene family (8); 18S gene (9); 18S, 25S and 5S genes (11).
Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit:	SSU gene SRS1 of a multigene family of at least 10 genes (4).
Urease:	Gene fragment (62).

Table 2. Soybean chloroplast genes

ATP synthase:	Gene atpH for subunit III of the CF-0 component (52); atpA, atpB, and atpE genes for alpha, beta and epsilon subunits of CF-1 component (52).
Cytochrome f of cyt b6/f complex:	Cyt F gene (52).
Cytoplasmic chlorophyll deficiency:	cyt-Y2 probably result of single point mutation in a regulatory portion of genome rather than in a structural gene (50).
Photosystem II thylakoid membrane:	32 kd protein <i>psbA</i> gene (52, 53, 54).
Ribosomal rRNA:	16S and 23S one copy and inverted repeat one copy (35, 51, 54).
Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit:	rbcl (52, 54).
Transfer RNAs:	tRNA ¹ -Leu, tRNA ² -Leu, tRNA ³ -Leu genes (37, 38); tRNA ^{2a} -Leu, tRNA ^{2b} -Leu genes (37); <i>trn</i> H gene (53); tRNA-Ile gene (51).

Table 3. Soybean mitochondria genes

Cytochrome b: Gene, low copy number (66).

Ribosomal rRNA: 18S gene (18); DNA rearrangement involving 5S gene (32).

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X. USDA Northern Soybean Germplasm Collection Report

February 21, 1986

In 1985, 51 accessions were added to the Soybean Germplasm Collection at Urbana, Illinois. Of these 51 accessions, 45 were from China, 1 from Japan, and 5 from South Korea.

The number of soybean germplasm accessions maintained at Urbana is listed below by maturity group.

Maturity group	Post-1944 public varieties	Old varieties	FC strains	1985 PI additions	PI total	Total	Percentage
000	1	3	1	0	89	94	1.3
00	14	5	4	0	330	353	4.8
0	15	7	6	6	829	857	11.7
I	24	23	3	16	1127	1177	16.1
II	40	26	6	14	1196	1268	17.3
III	31	38	13	10	1084	1166	15.9
IV	35	38	18	5	2321	2412	32.9
Total	160	140	51	51	6976	7327	100.0

The number of soybean germplasm accessions by country of origin is given below.

Country of origin	Old varieties	FC strains	PI strains	Total	Percentage
China	64	4	1256	1324	18.5
Japan	34	10	1035	1079	15.1
Korea	12	0	2044	2056	28.7
USSR	6	0	1809	1815	25.3
Other Asian	0	0	29	29	0.4
Europe	3	0	758	761	10.6
USA/Canada	20	36	0	56	0.8
Other*	1	1	15	17	0.2
Unknown	0	0	30	30	0.4
Total	140	51	6976	7167	100.0

*Africa, Australia, and Latin America.

In 1985, the wild soybean collection increased by 37 accessions, of which 27 were from China and 10 from Japan. The maturity group breakdown of these 1985 additions is as follows:

	000-00	0	I	II	III	IV	V	VI-VIII	IX	X	Total
China	0	2	6	6	8	5	0	0	0	0	27
Japan	0	0	0	0	0	0	7	0	3	0	10

Below is listed the total number of wild soybean accessions by country of origin and maturity group. Wild soybeans of maturity group V and later are grown at Stoneville, MS, by Dr. Thomas C. Kilen and stored at and distributed from Urbana.

Country of origin	Number of accessions by maturity group													Total	%
	000	00	0	I	II	III	IV	V	VI	VII	VIII	IX	X		
China	11	11	21	12	31	13	15	8	9	1	0	0	0	132	19.6
China, Taiwan	0	0	0	0	0	0	0	0	0	0	0	0	2	2	0.3
Japan	0	0	0	0	0	1	7	51	85	46	0	3	0	193	28.6
S. Korea	0	0	0	0	2	0	40	244	27	1	0	0	0	314	46.5
USSR	0	17	7	5	5	0	0	0	0	0	0	0	0	34	5.0
Total	11	28	28	17	38	14	62	303	121	48	0	3	2	675	100.0

There were 49 accessions of perennial *Glycine* species received in 1985, with the following breakdown by species: 4 *G. canescens*, 6 *G. clandestina*, 2 *G. falcata*, 11 *G. tabacina*, 20 *G. tomentella*, and 6 undescribed *Glycine* species. These accessions were generously donated by Dr. R. J. Lawn, CSIRO, Queensland, Australia. All of this seed was sent to the National Seed Storage Laboratory at Ft. Collins, Colorado, for storage until adequate facilities for maintenance of the perennial *Glycine* collection are provided.

The number of accessions maintained in the USDA perennial *Glycine* collection is as follows:

<i>G. argyrea</i>	0
<i>G. canescens</i>	1
<i>G. clandestina</i>	12
<i>G. cyrtoloba</i>	1
<i>G. falcata</i>	2
<i>G. latifolia</i>	6
<i>G. latrobeana</i>	0
<i>G. tabacina</i>	27
<i>G. tomentella</i>	17
Total	66

In 1985, a total of 347 seed requests for 21,956 seedlots were filled from the USDA Northern Soybean Germplasm Collection. U.S. and Canadian researchers requested 95% of these seedlots, with the remaining 5% requested from foreign researchers.

Annually updated checklists and other printed information are available from the curator. These include:

1. U.S. and Canadian Germplasm Variety Checklist (140 strains with maturity group and descriptive codes) January 1982;
2. U.S. and Canadian Public Variety Checklist (160 strains with maturity group and descriptive codes) January 1986;
3. FC and PI Strain Checklist (7,027 strains with maturity group) January 1986;
4. Wild Soybean Checklist (675 strains with maturity group) January 1986;
5. Wild Soybean Inventory (675 strains with maturity group and passport data) January 1986;
6. Genetic Type List (104 strains, up to T284, with genotype, phenotype, and origin information) January 1986;
7. Genetic Isoline List (183 Clark strains, 91 Harosoy strains, 11 Chippewa strains, 14 Wayne strains, and 1 Williams strain; with genotype, phenotype, and origin information) March 1975.

The second year of a wild soybean evaluation of 171 strains of Maturity Groups 000 through IV was completed in 1985. Information on 29 plant and seed traits (including seed composition) will be published in 1986.

A several-year project was begun in 1985 to survey the world's soybean germplasm and to obtain from wherever possible those accessions of soybean, wild soybean, and perennial *Glycine* species not already maintained in the USDA Soybean Germplasm Collection. In January 1986, 1,417 soybean accessions were generously donated by the National Institute of Agrobiological Resources,

Tsukuba, Japan. These accessions initially will be grown for observation and comparison in the summer of 1986. Additional requests for soybean germplasm will be made on an ongoing basis.

The USDA Germplasm Resources Information Network (GRIN) has updated information on 140 pre-1945 germplasm varieties, 160 post-1944 public varieties, and descriptive and evaluation data for FC and PI numbers through 266807D.

An inventory of the USDA Soybean Germplasm Collection will be published in 1986. This inventory includes all strains up to PI 476000, Maturity Groups 000 to X, and information on the country of origin and variety name. Copies of this publication will be available from the curator.

An international directory of soybean germplasm collections will be published in early 1986 in conjunction with the International Board for Plant Genetic Resources (IBPGR) and the International Soybean Program (INTSOY). This directory includes information on 87 soybean germplasm collections (cultivated, wild, and perennial species) in 43 countries. Copies of this publication will be available from INTSOY, University of Illinois, 113 Mumford Hall, 1301 West Gregory Drive, Urbana, Illinois, 61801 U.S.A.

R. L. Bernard, Curator
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XI. USDA Southern Soybean Germplasm Collection Report

February 1986 - Report on Germplasm V to X

	Total entries 1980	Total entries 1983	Total entries 1984	Total entries 1985
<hr/>				
V	1369	1520	1549	1550
VI	421	470	482	486
VII	314	334	346	349
VIII	266	285	297	303
IX	109	124	131	143
X	<u>136</u>	<u>151</u>	<u>154</u>	<u>158</u>
	2615	2884	2959	2989

Nineteen new additions for 1986.

Stoneville will grow 486 lines of germplasm VI in 1986.

1985 seed requests filled: 14,000 packets, to 8 countries, and to
18 states.

Calton Edwards

XII. RESEARCH NOTES

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1) Preliminary information on the *Rps* allele in the cultivar Harosoy.

The 'Harosoy' soybean cultivar was considered to be the universal susceptible for *Phytophthora megasperma* f. sp. *glycinea* when it was included in the differential host series for this pathogen (Haas and Buzzell, 1976). However, Moots (1982) reported that an *Rps* allele pair was present in Harosoy that conferred resistance to races 12 and 16. Harosoy is also resistant to races 18 and 19 but is susceptible to all other races 1-25 (unpublished results). The Harosoy *Rps* allele has not been characterized for assignment of a gene symbol and is referred to here as the *Rps?* allele. We have obtained preliminary results for *Rps?* in relation to other *Rps* loci.

Rps1: The cultivars 'Harosoy 63' (Harosoy (8) x Blackhawk), 'Mukden', and 'Union' carry the *Rps1-a* allele (Moots et al., 1983). Harosoy 63 is uniformly resistant to race 12 while Mukden and Union are susceptible. Both *Rps1-a* and *Rps?* are present in a homozygous form in Harosoy 63, hence *Rps?* must be at a different locus than *Rps1*.

Rps2: The *Rps2* gene in D54-2437 confers resistance to race 1 in hydroponic root inoculation (Kilen et al., 1974). L70-6494 (Harosoy (5) x D54-2437) carries the *Rps2* allele in a Harosoy background (R. L. Bernard, pers. comm.). When assayed by the hypocotyl technique used in this lab, L70-6494 is resistant to race 1 in screening for *Rps2* but is resistant to race 18 in screening for *Rps?*. The F_2 of L70-6494 x Harosoy does not segregate for resistance to race 18 (Table 1), thereby indicating that L70-6494 carries *Rps?* and *Rps2* at separate loci.

Rps3: PI 171442 is resistant to race 1 and is susceptible to race 12 (Keeling, 1982) as a result of *Rps3* being present (Kilen and Keeling, 1981). Since *Rps?* confers resistance to race 12 and not to race 1, these two races were used to screen for *Rps?* and *Rps3*. Half of an F_2 population of a backcross of *Rps3* to Harosoy was inoculated with each race (Table 1). The plants were resistant to race 12, indicating that the population was homozygous for the *Rps?* allele. A segregation ratio of 3R:1S was observed for race 1

inoculations which indicated that the population was heterozygous for the *Rps3* allele. These results indicate that the *Rps?* allele is not at the same locus as the *Rps3* allele.

Rps4 and *Rps5*: *Rps4* (Athow et al., 1980) confers resistance to race 18 (K. L. Athow, pers. comm.) as does *Rps?*. Likewise, *Rps5* (Buzzell and Anderson, 1981) tested in its original source T240 confers resistance to race 18 (unpublished results). Backcross material, resulting from crosses involving the *Rps4* and *Rps5* alleles and Harosoy, was crossed to the cultivar 'Kentland' (Northrup King S1492) which is susceptible to all known races. F_2 progeny of these crosses screened with race 18 gave 15R:1S ratios for both the *Rps4* and *Rps5* populations (Table 1). The results indicate that both populations possess two pairs of alleles at different loci that confer resistance to race 18. Hence, the *Rps?* allele is not at either *Rps4* or *Rps5*.

Rps6: The cultivar 'Altona', which carries the *Rps6* allele (Athow and Laviolette, 1982), is resistant to races 12, 16, 18 and 19 (Keeling, 1982). The F_2 progeny of a cross of Altona by Kentland screened with race 18 indicated a single *Rps* allele pair for race 18 resistance (Table 1). Further tests are needed to determine whether Altona carries *Rps?*.

Table 1. Results of screening F_2 populations for the presence of the *Rps?* allele and other *Rps* alleles

Population	Race	No. of plants		Ratio R:S	χ^2	P
		R	S			
L70-6494 x Harosoy	1	0	48	S	-	-
	18	100	0	R	-	-
(Rps3* x Harosoy)BC4	1	124	40	3:1	0.01	0.70
	12	199	1	R	-	-
(Rps4* x Harosoy) x Kentland	18	238	23	15:1	2.17	0.10
(Rps5* x Harosoy) x Kentland	18	264	25	15:1	2.84	0.05
Altona x Kentland	18	142	60	3:1	2.39	0.10

**Rps3* from PI 171442; *Rps4* from PI 86050; *Rps5* from T240 (L62-904).

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2) A comparison of soybean PAGE and starch gel electrophoretic patterns.

Researchers investigating isozymes in soybeans have employed both starch gel and polyacrylamide starch gel (PAGE) electrophoretic systems. Unfortunately, the banding patterns that have been observed when each of these gel systems is histochemically stained for a given isozyme can be quite different.

Most of the genetic work that has been done on soybean isozymes has been done on polyacrylamide starch gels (Gorman and Kiang, 1977) by Kiang and associates at the University of New Hampshire. However, researchers at the University of Guelph and at Iowa State University are also conducting genetic studies employing a starch gel system (Cardy and Beversdorf, 1984). To date,

Table 1. Comparison of observed isoxyme patterns from polyacrylamide (PAGE) and starch gels

Isozyme	Pattern designation		Number of bands [†]		Allele [‡]
	PAGE*	Starch [§]	PAGE	Starch	
ACP	M	A	3	2	Ap-b
	F	B	3	2	Ap-c
	S	C	3	2	Ap-a
DIA	1	A	11	9	Dial
	2	B	9	5	dial
GPI	3	A ^{§§}	4	6	§
	1	B	4	8	
IDH	5, 6	A	3	2	Idh1-b, Idh2-b
	7, 8	B	5	5	Idh1-a, Idh2-b
	1, 2	C	5	5	Idh1-b, Idh2-a
	3, 4	D	5	5	Idh1-a, Idh2-a
LAP	F**	A ^{§§}	2	2	Lapl-b
	S	B	2	2	Lapl-a
MPI	M	A	2	4	Mpi-b
	F	B	2	4	Mpi-c
PGD	1	A ^{§§}	3	4	-----
	2	B	2	4	-----
PGM	PF	A	3	5	Pgml-b
	PS	B	3	5	Pgml-a

[†]Refers to total number of bands visible when stained for the specific isozyme.

[‡]Refers to an allele pair associated with the difference between the stated patterns only.

[§]Although patterns coincide, PAGE has Pgml-a, and Pgml-b, codominant alleles; for starch gels these appear to behave in a dominant manner, pattern A dominant to B.

*PAGE patterns are from Gorman et al. (1982b).

**PAGE pattern from Kiang et al. (1985).

[§]Starch gel patterns from Cardy and Beversdorf (1984).

^{§§}Starch gel patterns from Rennie et al. (unpublished).

no published report exists that attempts to relate the observed banding patterns for each system, or to relate the genetic models, from one system to the other.

The isozymes that can be readily compared are: acid phosphatase (ACP); diaphorase (DIA); glucophosphate dehydrogenase (GPD); glucosephosphate isomerase (also known as phosphoglucose isomerase) (GPI); NADP-dependent isocitrate dehydrogenase (IDH); leucine amino peptidase (LAP); mannose-6-phosphatase (MPI); phosphoglucomutase (PGM); and 6-phosphogluconate dehydrogenase (PGD).

In order to compare the polyacrylamide/starch (PAGE) and starch gel systems, it is necessary to examine the results of running the same lines on both systems. The PAGE results were obtained from an extensive list compiled by Gorman et al. (1982b). The starch gel results were based on research done at the University of Guelph by Cardy (Cardy and Beversdorf, 1982), Hedges (pers. comm.) and by Rennie et al. (unpublished).

The alleles that are responsible for the differences between banding patterns on the PAGE system were taken from: Gorman et al. (1983), Gorman et al. (1982a), Gorman and Kiang (1978), Gorman and Kiang (1977), Kiang and Gorman (1985) and Kiang et al. (1985). The allele symbols were modified to those of Palmer et al. (1985).

There are alleles that have been identified employing the PAGE system that have not been related to banding patterns with the starch gel system. These include *Mpi-a* and alleles at the *Idh3*, *Dia2*, *Dia3* and *Pgm2* loci.

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87²⁴⁵ A study of linkage between markers and *Rps* loci conferring resistance to phytophthora root rot.

The identity of *Rps* alleles and loci conferring resistance to phytophthora root rot can ordinarily be determined by means of a hypocotyl screening procedure. However, if more than one *Rps* allele pair is included in a line, allele identification by this procedure can be very difficult. Several soybean/phytophthora breeding programs are including two or three *Rps* allele pairs in single lines, in order to provide resistance to all of the races of *Phytophthora megasperma* f. sp. *glycinea* (Pmg) in their area (Athow, pers. comm.).

The presence of a convenient marker system would be of benefit to workers in this area. Electrophoretic markers can be assayed readily by means of non-destructive techniques and their alleles are often co-dominant. These advantages make electrophoretic markers attractive to a breeder wishing to pyramid *Rps* alleles if a sufficiently close linkage exists between an *Rps* locus and a marker.

Using material from an *Rps* allelism study in which the parents differed for *Rps* alleles, electrophoretic markers, and hypocotyl color, a study was performed to determine if any of these markers would be suitable to aid in identification of *Rps* alleles. The *Rps* alleles were identified by hypocotyl inoculation. The electrophoretic procedures followed were essentially those of Cardy and Beversdorf (1984).

The isozymes and loci investigated were: aconitate hydratase (*Aco1*) (Rennie et al., 1986a); diaphorase (*Dial*) (Palmer et al., 1985); endopeptidase (*Enp*) (Rennie et al., 1986b); isocitrate dehydrogenase (*Idh1*) (Kiang and Gorman, 1985); and phosphoglucumutase (*Pgml*) (Palmer et al., 1985). In addition, the allele for flower/hypocotyl color (*w1* vs. *w1*) (linkage group 8) (Buzzell et al., 1977) was included, as it was segregating in these populations. Six loci that confer resistance to phytophthora root rot were tested: *Rps1-a*; *Rps3*; *Rps4*; *Rps5*; *Rps6*; and the *Rps* allele (*Rps?*) from Harosoy (see Rennie and Buzzell, 1986) (plus their respective recessive alleles).

Table 1. F₂ segregation data from soybean dihybrids for linkage analysis involving *Rps* loci and electrophoretic markers

Cross no.	Gene pair	AaB- [†]	AAB-	aaB-	$\frac{Ab}{ab}$	$\frac{Ab}{Ab}$	$\frac{ab}{ab}$	N	%R	S.E.
1	<i>Rps1</i> - <i>Aco4</i> * - <i>Dial</i>	108 100	41 55	34 40	37 23	10 20	12 12	242 250	53.3 48.0	4.7 3.9
2	<i>Rps3</i> - <i>Aco4</i> - <i>Idh1</i> - <i>Pgm1</i>	68 82 101	34 43 49	36 40 56	22 25 40	9 19 11	12 13 20	181 222 256	52.0 53.3 46.6	5.4 5.2 3.8
3	<i>Rps4</i> - <i>Aco4</i> - <i>Idh1</i>	70 75	37 42	33 43	26 35	7 12	16 13	189 220	>57 49.5	5.1
4	<i>Rps5</i> - <i>Idh1</i>	74	44	32	31	16	19	216	45.8	5.3
6	<i>Rps6</i> - <i>Aco4</i> - <i>Enp</i> * - <i>Pgm1</i>	78 86 76	31 34 34	33 41 51	28 39 31	14 16 19	18 12 18	202 224 230	52.5 53.6 53.4	5.2 4.1 4.2
7	<i>Rps?</i> - <i>Idh1</i> - <i>Pgm1</i>	84 102	55 34	45 39	30 26	14 19	15 18	243 238	47.5 52.2	4.9 5.0

[†]'A' refers to the *Aco4-a*, *Dial*, *Enp-a*, *Idh1-a*, or *Pgm1-a* alleles, 'a' refers to the other alleles at each locus. 'B' refers to the *Rps* alleles, 'b' refers to the *rps* alleles.

*Tentative gene symbols, papers have been submitted to Soybean Genetics Committee for approval.

Table 2. F₂ segregation data from soybean dihybrids for linkage analysis involving *Rps* loci and the *w1* locus for hypocotyl color, in linkage group 8

Cross no.	Gene pair	Phase*	A-B- [†]	A-bb	aaB-	aabb	N	%R	S.E.
1	<i>Rps1</i> - <i>w1</i>	C	150	49	41	16	256	47.5	4.5
2	<i>Rps3</i> - <i>w1</i>	C	154	57	56	13	280	>57	
3	<i>Rps4</i> - <i>w1</i>	C	141	50	48	17	256	50.0	4.7
5	<i>Rps5</i> - <i>w1</i>	R	183	64	59	14	320	44.7	4.4
7	<i>Rps?</i> - <i>w1</i>	C	149	50	43	13	256	51.4	4.7

*C - coupling, R - repulsion.

[†]'A' refers to the *Rps* allele, 'a' to the *rps* allele. 'B' refers to the *w1* allele, 'b' refers to the *w1* allele.

The crosses involved were:

1. OX20-8 (*Aco4-b*, *dial*, *w1*, *Rps1*) x Kentland (*Aco4-a*, *Dial*, *w1*, *rps1*);
2. (*Rps-3* x Harosoy)-BC-5 (*Aco4-b*, *Idh1-a*, *Pgml-a*, *w1*, *Rps3*) x Kentland (*Aco4-a*, *Idh1-b*, *Pgml-b*, *w1*, *rps3*);
3. (*Rps-4* x Harosoy)-BC-5 (*Aco4-b*, *Idh1-a*, *w1*) x Kentland (*Aco4-a*, *Idh1-b*, *w1*);
4. (*Rps-5* x Harosoy)-BC-7 (*Idh1-a*, *Rps5*) x Kentland (*Idh1-b*, *rps5*);
5. L62-904 (*w1*, *Rps5*) x Harosoy (*w1*, *rps5*);
6. Altona (*Aco4-b*, *Enp-a*, *Pgml-a*, *w1*, *Rps6*) x Kentland (*Aco4-a*, *Enp-b*, *Pgml-b*, *w1*, *rps6*);
7. Harosoy (*Idh1-a*, *Pgml-a*, *w1*, *Rps?*) x Kentland (*Idh1-b*, *Pgml-b*, *w1*, *rps?*).

Percentage recombination was obtained by the maximum likelihood method of Allard (1956). Each of the *Rps* loci segregated independently of the electrophoretic markers with which they were tested (Table 1). In addition, each *Rps* locus segregated independently of the *w1* locus in linkage group 8 (Table 2).

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I) Comparison of inheritance of several agronomic characters between *Glycine max* x *G. soja*, *G. max* x *G. gracilis*, and *G. max* x *G. max*.

In 1984, parents, F_1 , F_2 , and F_3 populations of three crosses of *Glycine max* x *G. soja*, *G. max* x *G. gracilis* and *G. max* x *G. max* had been planted simultaneously for comparison of the inheritance of several agronomic characters of the above three different soybean crossing combinations. Performance of lines or cultivars of different species used as parents can be shown in Table 1.

Table 1. Performance of cultivars or lines of different soybean species used as crossing parents (1984, Harbin)

Species	Cultivars or lines used	Growth period (days)	Weight of 100 seeds (g)	Protein (%)	Oil (%)
<i>Glycine soja</i>	Lon 49-6416	126	1.11	49.3	9.16
<i>Glycine gracilis</i>	Booli Semi-wild	128	9.53	37.9	17.4
<i>Glycine max</i>	Don Non 33	128	26.2	42.9	20.7
<i>Glycine max</i>	Ha 75-5396	122	19.1	42.3	18.9
<i>Glycine max</i>	Haju 781	110	26.1	36.2	21.3

These results reveal that:

1. The sequence of magnitude of variation of the agronomic characters of F_3 population is: *G. max* x *G. soja* > *G. max* x *G. gracilis* > *G. max* x *G. max*. Selection potential for new types is evidently larger in progenies of *G. max* x *G. soja* as well as *G. max* x *G. gracilis* combinations.
2. High protein content and prolific podding individuals occur more frequently in progenies of *G. max* x *G. soja* combination, while more erect types can be selected out from progenies of *G. max* x *G. gracilis* combination. New soybean types with some noticeable promising characters can be selected out from crosses with *G. soja* or *G. gracilis* as parent. Such types are valuable parents in soybean breeding programs although they may not be acceptable for commercial growing.

Table 2. Genetic performance of F₃ progeny lines of crosses *G. max* x *G. soja*, *G. max* x *G. gracilis*, and *G. max* x *G. max* (1984, Harbin)

Agronomic characters	Combination	Variation			Expected genetic advance (15%)		Gene effect	
		Mean value	Range	PCV (%)	GCV (%)	GS	RGS(%)	(d) (h)
Seed weight per plant	<i>G. max</i> (Don Non 33) x <i>G. soja</i> (I) (Lon 49-6416)	22.7(g)	5-68(g)	58.98	38.59	21.78	55.50	1.2 16
	<i>G. max</i> (Ha 75-5396) x <i>G. gracilis</i> (II) (Booli Semi-wild)	18.1	4-45	42.27	24.94	14.33	49.48	1.1 12
	<i>G. max</i> (Haju 781) x <i>G. max</i> (III) (Don Non 33)	22.1	6-40	31.8	12.98	8.27	31.32	0.2 6
Number of seeds per plant	I	346.2	38-1127	61.31	47.32	507.99	81.36	377 682
	II	139.4	38-313	32.77	18.69	93.29	40.78	36 64
	III	93.0	30-194	33.05	15.00	44.33	37.25	9 10
Weight of 100 seeds	I	6.65(g)	3-12(g)	27.96	26.67	1.45	19.11	19.0 6.0
	II	13.1	6-18	16.15	15.43	2.57	18.82	5.0 0.3
	III	24.0	12-34	14.2	9.11	4.73	20.51	1.0 0.3
Protein content	I	44.7(%)	38-54(%)	6.84	4.44	3.18	6.53	3.35 2.5
	II	42.3	34-53	10.21	9.78	2.98	4.60	2.6 1.2
	III	41.0	35-49	9.39	8.73	2.11	5.11	3.2 2.2
Oil content	I	14.1(%)	10-17(%)	12.34	6.38	1.40	9.64	5.6 4.3
	II	17.6	13-21	8.59	7.42	1.55	8.57	0.7 0.9
	III	20.0	16-24	9.36	6.65	0.85	4.2	0.1 0.2

3. Additive gene effect is the main gene effect for protein content, oil content, and weight of 100 seeds, and they are much higher in *G. max* x *G. soja* and *G. max* x *G. gracilis* combinations; the gene effect of seed weight per plant and number of seeds per plant is the most dominant effect and is also much higher in those two crosses.
4. *G. max* x *G. soja* and *G. max* x *G. gracilis* combinations take more generations for segregation than *G. max* x *G. max* combination, and their populations need more generations to have a certain amount of homozygous individuals. Therefore, in soybean breeding programs, intensive selection should be postponed to later generations when *G. soja* or *G. gracilis* is used as parent to cross with *G. max*.
5. Expected genetic advance of protein content, seed weight, and number of seeds per plant both on actual value and on percentage are higher in *G. max* x *G. soja* and *G. max* x *G. gracilis* combinations. This means such combinations are very promising for selecting progenies with higher protein and higher seed yield.

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12-¹⁴⁵ Screening soybean germplasm for seed longevity under tropical environments.

Field stands of soybeans are usually poor in tropical environments due to seed deterioration in ambient storage. Seed deterioration begins when soybean plants reach physiological maturity in the field (Delouche, 1981). The final quality of the planting seed is affected by weather conditions during seed maturation and by temperature and relative humidity during seed storage.

The cost of controlling temperature and relative humidity in seed storage is out of reach to the farmers in developing countries. Therefore, one possible way to help improve soybean seed quality in tropical regions is to instruct farmers of the importance of timely harvest of the planting seed, and to provide them with soybean varieties capable of maintaining prolonged seed viability in ambient storage.

The research reported here was undertaken to evaluate the rate of seed deterioration in ambient storage in a group of 48 soybean varieties obtained by INTSOY from tropical countries.

Materials and methods: The 48 varieties studied originated from Colombia, Nigeria, Philippines, Senegal, Sri Lanka, Taiwan, and Vietnam. All accessions were grown in the field to produce high quality seed in Puerto Rico in 1983, and at the ICA Experiment Station in Palmira, Colombia, in 1984. Plants were harvested at physiological maturity (plants showing 50% of yellow pods) and allowed to dry slowly under shade conditions; after threshing, the seeds were further dried to about 10% moisture. The dried seeds were selected for uniformity and healthy appearance and then packed in cloth bags; these were placed at room temperature in two environments. One of the environments was the ICA Experiment Station at Palmira, where the average air temperature varies between 18 and 28°C and the relative humidity varies between 75 and 80%. The other environment was the ICA Experiment Station at Monteria, in the northern coastal area, where the average temperature varies between 23 and 32°C and the relative humidity between 82 and 90%.

Seed deterioration was measured in each accession at each environment through germination tests conducted at two-month intervals in Palmira and at one-month intervals in Monteria. Varieties 'Bossier' from the U.S. and 'Tunia' from Colombia were used as checks in the experiment. The average percent

germination was determined for each accession, and the Coefficient of Variability (CV) of this average was calculated for each test. At each environment, the experiment was conducted in 1984 and 1985.

Results and discussion: At zero months of storage in 1984, the average seed viability was 97% in Palmira and 94% in Monteria, and the CV values were 2 and 9%, respectively. At two months of storage, average seed viability was 96% in Palmira and 86% in Monteria, and the CV values were 4 and 16%, respectively. At four months of storage, seed viability in Palmira decreased to 94% and the CV value increased to 6%, while in Monteria seed viability dropped to 16% and the CV jumped to 136%. These results indicate that seed deterioration was slow and uniform for all genotypes in Palmira, while in Monteria seed deterioration occurred at a fast rate with large differences among genotypes. Results observed in 1985 were similar to those of 1984. In both years, germination tests were conducted for more than 12 months in Palmira but only during five months in Monteria where most genotypes had lost seed viability at this time. Since the initial seed viability was similar in both environments, the conclusion is that higher temperature and relative humidity in Monteria induce fast seed deterioration in susceptible genotypes.

One group of four genotypes consistently appeared to surpass others in both years in Monteria, showing seed viability between 30 and 85% after four months of storage. These are shown in Table 1.

Table 1. Seed viability and other seed traits of promising genotypes compared with checks at four months of storage in Monteria

Line or variety	Germination % at four months		Seed color	Weight of 100 seed, g	Origin
	1984	1985			
MTD-10	85	75	Yellow	13.0	Vietnam
TGm 737p	77	80	Black	6.5	Nigeria (IITA)
G2120	58	46	Yellow	6.5	Taiwan (AVRDC)
TGx 297-192C	30	61	Black	9.0	Nigeria (IITA)
Bossier (check)	0	9	Yellow	20.0	U.S.A.
Tunia (check)	3	0	Yellow	22.5	Colombia

Line TGM 737p was selected in IITA for its storability performance in studies conducted by Wien and Kueneman (1981) and by Kueneman (1983) using accelerated aging tests. This line performed equally well in our studies under ambient storage. It appears, according to data of Table 2, that seed longevity may be associated with small seed size; if this observation is genetically confirmed, plant breeders may need to look into linkage or pleiotropic effects when attempting to improve the seed longevity trait. Researchers interested in the above promising lines may obtain seed from INTSOY.

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Heritability estimates for seed quality traits in soybeans.

Breeding programs with primary emphasis on yield and resistance to diseases are in progress at this center since 1967-68. Rapid strides have since been made in this direction with breeding and release of several high-yielding soybean varieties, viz: Ankur, Alankar, Shilajeet, PK-262, PK-327, PK-308, and PK-416. However, still a constraint to expansion of soybean cultivation in tropics seems to be deterioration of seed quality in storage. A few Indian soybean strains grown by farmers (Kalitur and T-49) have been identified as potential donors to improve soybean seed storability and are being used in our breeding programs. The present investigation deals with estimation of heritability for seed storability, impermeability, and the electrical conductivity of seed leachate in soybean.

Materials and methods. F_2 and F_3 generations of some crosses involving contrasting parental cultivars were evaluated for seed storability, seed impermeability, and electrical conductivity (EC) of seed leachate. Storability was measured as germinability of seeds after accelerated aging at 40°C and 100% humidity for 96 hrs (slightly modified after Byrd and Delouche, 1971). Seed impermeability was determined by soaking seeds for 24 hrs in water. In both the above tests, 50 seeds/plant were used in each determination. For EC, 1 g uncracked seeds/plant were surface sterilized in 0.1% mercuric chloride for 10-15 min, then soaked in 100 ml distilled water for 12 hrs. The leachate was used for measuring EC on a conductivity meter (Matthews and Bradnock, 1968).

Heritability was estimated through parent-offspring correlation technique (Bassett and Woods, 1978) and parent-offspring regression technique (Lush, 1948).

Results and discussion. Six parental varieties had the following features with respect to seed quality.

Variety	Storability	Hard seeds (%)	Electrical conductivity (m mhos/cm) at 25°C, 5 month old seeds
Bragg	Poor	Normal (0-3%)	High (25-37)
Bragg-black seed	Poor	Normal (0-18%)	Medium (16-24)
Kalitur	Good	Normal (no hard seeds)	Medium-high (18-30)
Ankur	Good	Normal (1% hard seeds)	High (25-35)
WT-125	Good (due to hard seeds)	Hard seeded (>.90% hard seeds)	Low (3-10)
<i>Glycine formosana</i> (wild soybean)	Good (due to hard seeds)	Hard seeded (>.70% hard seeds)	Low (6-16)

Narrow sense heritability estimates for the different seed quality components are given in Table 1.

Table 1. Narrow sense heritability estimates (%) for seed quality characters in different crosses in soybean

Crosses	Storability	
	Parent-offspring correlation technique	Parent-offspring regression technique
	(%)	(%)
Bragg x Kalitur	39.73	53.9
Bragg x Ankur	23.26	47.3
<u>Impermeability</u>		
Bragg x WT-125	5.47	5.3
Bragg x <i>G. formosana</i>	22.50	22.4
Bragg-black seed x WT-125	12.33	19.1
Bragg-black seed x <i>G. formosana</i>	48.59	75.4
Kalitur x WT-125	16.53	18.6
Kalitur x <i>G. formosana</i>	29.67	34.1
Ankur x WT-125	25.86	39.1
Ankur x <i>G. formosana</i>	8.53	8.0
<u>Electrical conductivity</u>		
Bragg x WT-125	14.46	15.9
Ankur x WT-125	12.26	12.3

For storability/germinability, the narrow sense heritabilities estimated through parent-offspring regression method were 53.9% and 47.3% in the crosses Bragg x Kalitur and Bragg x Ankur, respectively. The corresponding estimates through parent offspring correlation method were 39.7% and 23.26%. These estimates were close to the narrow sense heritabilities reported by Green and Pinnell (1968), Green et al. (1971) and Singh (1984) in soybeans. Singh et al. (1978) obtained moderately high heritability (74.64-80.59%) and suggested possible improvement for seed germination through hybridization and selection. Relatively high narrow sense heritability estimates reported here indicated that selection may be effective and it should be possible through selection to increase the germinability.

For impermeability, narrow sense heritability estimates ranged from 5.3 to 75.4%. The cross Bragg-black seed x *G. formosana* showed the highest narrow sense heritability of 75.4% through parent offspring regression method and 48.59% through parent offspring correlation method, whereas the cross Bragg x WT-125 and Ankur x *G. formosana* revealed 5.3% and 8.0% narrow sense heritability through regression method and 5.47% and 8.53% through correlation method, respectively. The results indicated that seed impermeability was a highly heritable character in the cross Bragg-black seed x *G. formosana*. This observation was in close agreement with those of Shahi (1980), who observed high broad sense heritability (80-90%) in three crosses of soybean, and suggested that it may not be much influenced by the environment. However, in most of the crosses studied here, the heritability estimate was low, implying a greater role of environment. Archavaleta and Snyder (1981) have also suggested that environment played a fairly great role in rendering soybean seeds impermeable to water.

Low narrow sense heritability estimates for electrical conductivity (12.26-15.90%) indicated that it would be difficult to use it as reliable component of seed quality. Kueneman and Wien (1981) and Gumisiriza and Kueneman (1982) have expressed the opinion that use of seed leachate characteristics for vigor assessment may not be ideal.

In conclusion, we suggest that it is possible to improve soybean seed storability rather more easily than to manipulate seed leachate characteristics in order to breed soybean varieties for the tropics where seed quality deteriorates rapidly under ambient storage conditions.

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1) Response of soybean (*Glycine max* (L.) Merrill) to foliar application of some growth regulators and in combination with urea and potash.

Introduction: The concept of foliar nutrition and its relationship with yield is not new. Nutrients, especially the micronutrients when applied as foliar spray, exert pronounced influence on plant growth and yield. Such micronutrients are in use for improving the growth and yield of crops. Narula et al. (1967) and Ashour (1971) reported the use of micronutrients as foliar application in wheat. In soybean, there were reports of improvement of yield with foliar nutrition (Barthakur, 1980). The present investigation was undertaken to find out the effect of growth regulators alone and in combination with nitrogen and potash on growth and grain yield of soybean.

Materials and methods: The experiment was conducted with soybean Var. 'JS 2' in 1984 at Assam Agricultural University, Jorhat, situated at 26°47' N. Latitude and 94°12' E. Longitude on sandy loam soil pH 5.2 in 3 randomized block design. Fertilizers were applied at 20:60:40 N, P₂O₅ and K₂O in kg/ha, respectively, as basal application. The crop was sown on 31 July in rows 30 cm apart and plant-to-plant 7 cm apart, and was harvested on November 7, 1984. Growth regulator Bardhak 20 ppm, Planofix 20 ppm and Selmen 20 ppm, (all these chemicals contain naphthylene acetic acid as active ingredient) Tracel - 2 micronutrient mixture at 5 g/l, Urea and M.O.P. at 3% (300 g/10 L) were used alone and in combination. A control with water spray was also maintained.

The plant foliage was sprayed once at 50% flowering. Observations were recorded on plant height, total leaves/plant, number of branches/plant, number of pods/plant, number of flowers/plant, and the grain yield.

Results and discussion: The sprays of chemicals failed to produce any significant difference in plant height and number of branches per plant, but did produce significant differences between treatments in number of flowers, and number of pods/plant. Grain yield was significantly affected (Table 1, T₅). The increase grain yield due to Bardhak alone with nitrogen and potash (T₅) was recorded (2131.67 kg/ha) followed by (T₆) Planofix in combination with nitrogen and potash produced 1992.33 kg/ha. The increase in yield may be attributed to combined effect of growth regulators and nutrients. There is a possibility that plant sex may also affect their response to combined action

Table 1. Effect of foliarnutrition on soybean on yield and yield components, 1984 (rainy season)

Treatments ^a	Plant height (cm)	No. of branches/plant	No. of flowers/plant	No. of pods/plant	Grain yield (kg/ha)
Bardhak (T ₁)	52.33	3.67	152.00	67.33	1066.33
Planofix (T ₂)	48.67	3.33	148.67	91.67	937.00
Salmen (T ₃)	47.00	3.00	155.33	85.33	1068.67
Tracel - 2 (T ₄)	57.00	3.66	157.67	85.00	1251.67
Bardhak + 3% U + K each (T ₅)	55.67	4.67	170.67	112.66	2131.67
Planofix + 3% U + K each (T ₆)	54.33	3.36	158.66	112.33	1992.33
Salmen + 3% U + K each (T ₇)	44.33	3.00	156.33	69.00	900.00
Tracel - 2 + 3% U+K each (T ₈)	47.33	3.00	144.00	73.33	911.00
U + K 3% each (T ₉)	51.30	3.00	149.00	85.33	983.33
Control (T ₁₀)	47.67	3.33	128.67	56.67	594.33
C.D. at 5%	NS	NS	NS	21.11	68.38

^aU = Urea, K = Potash.

of nutrients and growth regulators. Retention of flowers in treated plants in comparison to control is another factor by which the yield in pod and grain may have increased. Total dry weight of biomass is another indication of the response of applied nutrients. The yield of air dry mass of the male hemp plant was found to be higher due to foliar spray with Cu + GA₃ (Bakardjieva and Ivanova, 1970). Similar results of increased grain yield ranging from 0.94 t - 1.23 t/ha in soybean, cv. Hill, were obtained by foliar application of 40 ppm TIBA to 30 days old plants (Krishnamurthy and Gowda, 1977). Rajput and Sexana, 1973, also obtained results conforming to the above.

The retention of flowers and pods, which may be attributed to prevention of abscission, was already known (Addicott and Hynch, 1951). From the evidence discussed above, it is clear that the combined effect of foliar nutrition of growth regulators and urea plays a vital role by preventing abscission as well as balanced growth regulating in higher yield.

The present experimental yield was low because of late sowing due to incessant rain. It was established that variety 'JS 2' showed better performance in early (June) sowing (Sarmah and Kalita, 1984).

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2) Effect of mulching on seedling emergence and yield of soybean

Abstract. Experiment carried out with different materials for two years revealed the beneficial effects of mulching on seedling emergence as well as yield. The average increase in seedling emergence over control (no mulching) was 97.3, 53.1, 35.7, and 28.6% in plots mulched with paddy straw, wheat straw, paddy husk, and wheat husk, respectively. Mulching with paddy straw and wheat straw resulted in 55.5% and 44.1% increase in grain yield, respectively, over no mulching. The reasons for the beneficial effects of mulch in seedling emergence and increase in grain yield is discussed.

June-July is the recommended time for rainy season sowing of soybean in Assam. Seedling emergence is, however, badly hindered if there is heavy shower within 72 hrs of sowing, because of formation of hard crust on the top layer. Seeds may also rot due to accumulation of water coupled with high temperature. Mulching has been reported to have beneficial effects in improving seedling emergence through its dual effects in preventing crust formation and reducing soil temperature (Kaul and Sekhon, 1977). A trial was undertaken to study the effects of different mulches on seedling emergence and yield of soybean at Jorhat, which receives heavy rainfall during June and July (more than 300 mm in each month).

Materials and Methods: The experiment was laid out consecutively for two years, 1978 and 1979, in randomized block design with 4 replications. Seeds of soybean var. 'JS 2' were sown on 5 July 1978 and 5 July 1979 on a sandy loam soil with pH 5.2. The crop was fertilized with 20, 80, and 60 kg/ha of N, P, and K, respectively. Half of the graded dose of N was applied at sowing, and the remaining half at the time of first weeding. Seeds were inoculated with *rhizobium* culture at the rate of 8 g/kg of seeds, before sowing. The gross plot size was 4 x 3 m. Six rows of 4 m length were made in each plot at the row distance of 45 cm. Within the rows, seeds were dibbled at 8 cm apart. Thus, a total of 300 seeds were dibbled in each plot. The

different kinds of mulches used were paddy straw, wheat straw, paddy husk, and wheat husk. In control plots, no mulching was done. Two hand weedings were done at 15 days and 35 days after sowing. At the time of second weeding, a light earthing up was done.

Results and Discussion: Mulching with paddy straw resulted in the highest percentage of seedling emergence, 53.16% for 1978 and 53.75% for 1979, respectively, and were significantly superior to other mulching treatments as well as control (Table 1). In control, the emergence was 24.43% and 29.75% for the years 1978 and 1979, respectively. Mulching with wheat straw, paddy husk, and wheat husk also had significant increase in emergence compared with control, and were at par among themselves for the year 1978. However, for the year 1979, all the treatments significantly differed from each other. The order of emergence for both the years with different mulching materials was paddy straw > wheat straw > paddy husk > wheat husk > control (no-mulching). The average increase in emergence for two years over control was 97.30, 53.12, 35.73 and 28.57%, for mulching with paddy straw, wheat straw, paddy husk, and wheat husk, respectively. Thus, there was almost two-fold increase in emergence when paddy straw was used as mulching material and one and a half-fold increase with wheat straw compared with control.

Table 1. Effect of different mulches on seedling emergence and yield of soybean

Treatment (mulch used)	Seedling emergence (%)			Grain yield (g/ha)		
	1978	1979	Mean	1978	1979	Mean
Paddy straw	53.16	53.75	53.45	25.80	22.20	24.00
Wheat straw	44.45	38.51	41.48	24.45	20.02	22.23
Paddy husk	37.37	36.18	36.77	21.51	19.67	20.59
Wheat husk	36.60	33.06	34.83	22.40	18.67	20.53
Control (no mulch)	24.43	29.75	27.09	14.10	16.77	15.43
C.D. (0.05)	10.75	2.30		7.40	2.87	

Mulching resulted in significant increase in the grain yield for both the years compared with control (Table 1). The highest grain yields of 25.80 g/ha and 22.20 g/ha were recorded in plots mulched with paddy straw for the years 1978 and 1979, respectively. Mulching with wheat straw and paddy husk also

produced significantly higher yield compared with control for both the years. In 1978, there was no significant difference in yield due to different mulching treatments among themselves. Significant increase in yield, compared with other mulching treatments and control were, however, recorded in plots mulched with paddy straw in 1979. No difference in yield due to mulching with wheat straw, paddy husk, and wheat husk could be noticed in this year. Kaul and Sekhon (1977) reported that there was a spectacular increase in yield of soybean 'Bragg' in the amount of 159.6% in plots treated with *rhizobium* and mulched with whole wheat straw compared to noninoculated and nonmulched (control) plots.

The monsoon season (June to August) in Assam is characterized by cloudy weather with high humidity (above 80%). Temperature and precipitation increase with the advance of the season. The rainy days vary from 18 to 20 days in a month during these months. The annual rainfall (average of 5 years, 1976 through 1980) was 309 mm and 388 mm for the months of June and July, respectively. The average maximum and minimum temperature for the corresponding periods were 31.5°C and 24.3°C for June, and 32.2°C and 25.0°C for July, respectively. Significantly higher percent of seedling emergence and yield could be achieved for both the years, through mulching treatments. Despite heavy rainfall during sowing as well as growth periods, it appears that mulching contributed to seedling emergence by preventing crust formation and reducing the soil temperature.

A mid-summer temperature of 23.9°C to 25.0°C is optimum for soybean plant growth (Martin et al., 1976). The average temperature reported for Jorhat conditions appears to be in the higher side and this might have inhibited seedling emergence. It is known that *rhizobium* cannot flourish in high temperature. Kaul and Sekhon (1977) reported that mulching caused a considerable reduction in soil temperature (about 10°C) and suggested that this might have helped in better establishment and activity of *rhizobium*. Tilak (1976) reported that mulching helped in inducing nodulation of soybean 'Bragg'. In the present study, paddy straw contributed an increase of seedling emergence (97.3%) and yield (55.5%) over control. This probably was due to the dual beneficial effects of mulching which prevented crust formation and reduced the soil temperature.

The increase in seedling emergence, as a result of mulching, has considerable significance for heavy rainfall areas. A high correlation ($r = 0.994$) was found between seedling emergence and yield. It may be mentioned that, in

the present study, extremely low seedling emergence (27%) was noticed in nonmulched plots. If the increase in emergence could be enhanced substantially by use of mulches, as found in the present study, a good plant stand in the field could reasonably be maintained, which ultimately will result in high production.

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1) Genetic variability, interrelationships and path coefficient analysis of seed technological traits in soybean under different cropping systems.

Soybean is generally cultivated in India as a sole or monoculture crop. However, its intercropping with maize is a common practice in some hilly areas of northern India. The practice aims at (1) insuring against total crop failures under abnormal weather conditions, (2) increasing total productivity for unit land area, and (3) equitable and judicious utilization of land resources and farming inputs. Seed technological traits are important and must be taken into consideration in the soybean improvement program. Therefore, it becomes essential to know the effect of cropping systems on the genetic variability, interrelationships, and path coefficient analysis of seed technological traits. Information obtained will eventually help in a breeding program aimed at evolving superior genotypes required for different cropping systems.

Materials and methods. The material for the present study consisted of 50 diverse genotypes of soybean, including five recommended varieties. These were grown in a randomized block design with three replications during 1981 under two sets of cropping systems, monoculture and intercropping with maize. Each entry in monoculture as well as in association with maize ('Early Composite', a locally recommended variety) as intercrop (one row of soybean between two rows of maize 75 cm apart) was grown in a single 3 m long row in each replication. In monoculture, row-to-row distance was 45 cm. The agronomic practices followed under both the cropping systems were the same as recommended for this crop. The genotypes were harvested and the observations were recorded on seed quality traits such as 100-seed volume (cc), seed specific gravity index (%), seed germination (%) and non-hard seeds (%) from the seed samples obtained from each genotype. Phenotypic and genotypic coefficients of variation, heritability in the broad sense, and expected genetic advance ($K = 2.06$) as % of mean, correlation coefficients, and path coefficients were computed according to standard procedures.

Results and discussion. Analysis of variance indicated significant differences among genotypes for seed technological traits. Range values were slightly higher for seed germination, non-hard seeds and 100-seed volume under monoculture and for seed specific gravity index under intercropping (Table 1).

The mean values of 100-seed volume, seed germination and non-hard seeds were comparable under both the cropping systems. However, seed specific gravity index was higher under intercropping than monoculture. Gupta et al. (1981) observed that intercropping provided the favorable environment for the expression of high seed specific gravity index and, in turn, high oil content. However, contrary to the present findings, they reported decrease in germination and hard seeds.

The values of phenotypic and genotypic coefficients of variation were high for seed specific gravity index and 100-seed volume under both the cropping systems (Table 1). The magnitude of these parameters was very low for the remaining characters. These estimates were comparable under both cropping systems except for seed specific gravity index, which was higher under monoculture environment. The estimates of phenotypic and genotypic coefficients of variation for seed specific gravity index were also found to be higher under monoculture than intercropping (Gupta et al., 1982a).

The values of genetic parameters such as heritability and genetic advance were higher for 100-seed volume and seed specific gravity index and low for laboratory germination and non-hard seeds. The magnitude of heritability and genetic advance for laboratory germination was higher under monoculture than intercropping (Table 1). The estimates were comparable in the remaining three traits. The results suggested little or no influence of the cropping system on the heritability and genetic advance of the seed technological traits. By contrast, Gupta et al. (1982b) observed substantial effect of the cropping pattern on the magnitude of genetic parameters of seed technological traits. The estimates were higher under monoculture than intercropping.

The association of different seed technological traits with seed yield at phenotypic and genotypic level revealed that the interrelationships were nonsignificant. The only exceptions were that of positive interrelationship of germination with non-hard seed under both the cropping systems, negative association of 100-seed volume with germination under intercropping and positive interrelationship of 100-seed volume with seed yield/plant under intercropping. As observed in the present study, Garg (1979) reported that hard seeds had no association with seed yield. The results of Smith and Weber (1968) were also in accordance with the present findings, where they had reported the absence of association between the seed specific gravity index and seed yield/plant. Unlike the present study, Rana et al. (1982) observed positive association between 100-seed volume and seed yield/plant under monoculture system of cropping.

Table 1. Range, mean, phenotypic and genotypic coefficients of variation, heritability and genetic advance for seed technological traits in soybean under two cropping systems

Character	Range		Mean \pm S.E.		Phenotypic coefficient of variation (%)		Genotypic coefficient of variation (%)		Heritability (%)		Genetic advance as % of mean (%)	
	M ^a	I ^b	M	I	M	I	M	I	M	I	M	I
100-seed volume (cc)	9.00-26.57	7.33-22.67	12.33 \pm 0.01	13.03 \pm 0.01	20.40	22.59	21.12	19.31	74.94	72.12	37.63	34.00
Seed specific gravity index (%)	41.67-68.67	52.67-88.00	20.11 \pm 0.23	28.22 \pm 0.31	28.72	18.81	20.41	13.35	85.01	84.53	50.24	32.83
Seed germination (%)	83.33-99.33	88.33-100.00	94.49 \pm 0.17	95.57 \pm 0.09	5.80	3.99	2.41	1.25	17.23	9.78	2.06	0.80
Non-hard seeds (%)	70.43-88.00	83.50-88.00	85.10 \pm 0.13	86.26 \pm 0.03	5.84	3.17	2.68	2.00	21.14	39.95	2.54	2.60

^aM = Monoculture.

^bI = Intercropping.

Table 2. Association of seed technological traits with seed yield in soybean under two cropping systems

Character	Seed specific gravity index (%)		Seed germination (%)		Non-hard seeds (%)		Seed yield/plant (g)	
	M ^a	I ^a	M	I	M	I	M	I
100-seed volume (cc)	P ^b	-0.105	-0.008	-0.238*	0.067	-0.153	0.113	0.244*
	G	-0.019	0.050	-0.804	0.162	-0.205	0.153	0.368
Seed specific gravity index (%)	P		0.141	0.078	-0.173	0.106	-0.192	0.005
	G		-0.516	0.135	-0.542	0.211	-0.282	0.002
Seed germination (%)	P				0.618**	0.251*	0.101	0.021
	G				0.836	0.526	0.303	0.096
Non-hard seeds (%)	P						0.060	0.036
	G						0.008	0.181

^aM = monoculture; I = intercropping.^bP = phenotypic; G = genotypic.

*P < 0.05.

**P < 0.01.

Table 3. Direct and indirect effects of seed technological traits on seed yield in soybean under two cropping systems

Character	Effect via											
	100-seed volume (cc)			Seed specific gravity index (%)			Seed germination (%)			Non-hard seeds (%)		
	M ^a	I ^a		M	I		M	I		M	I	
100-seed volume (cc)	P ^b 0.116 ^c	0.272		0.001	-0.002		-0.001	-0.023		0.003	-0.009	
	G 0.266	1.419		0.006	-0.003		0.050	-1.100		-0.169	0.052	
												0.368
Seed specific gravity index (%)	P -0.002	-0.029		-0.185	0.022		-0.014	0.006		0.007	0.006	
	G -0.005	-0.158		-0.330	0.025		-0.512	0.184		0.565	-0.053	
												0.005
Seed germination (%)	P -0.002	-0.065		0.026	0.002		0.103	0.070		-0.028	0.014	
	G 0.013	-1.141		0.170	0.003		0.992	1.367		-0.872	-0.133	
												0.096
Non-hard seeds (%)	P 0.008	-0.041		0.032	0.002		0.064	0.017		-0.044	0.058	
	G 0.043	-0.291		0.179	0.006		0.830	0.719		-1.044	-0.253	
												0.181

^aM = monoculture; I = intercropping.

^bP = phenotypic; G = genotypic.

^cUnderlined figures denote the direct effect.

*P < 0.05.

The results indicated that cropping system has little influence in altering the nature and magnitude of association between the seed technological traits.

The path coefficient analysis of different seed technological traits revealed that the direct phenotypic effects of 100-seed volume and seed germination were positive under monoculture (Table 3). However, under intercropping, the direct effect of 100-seed volume alone was substantial. The indirect effects of these characters were negligible. Similarly, the direct and indirect effects of non-hard seeds towards seed yield were negligible. The negative, but nonsignificant association of seed specific gravity index with seed yield ($r = 0.192$) was mainly because of the substantial negative direct effect of seed specific gravity index under monoculture. In case of intercropping, the trend of phenotypic and genotypic direct and indirect effects was almost similar to monoculture.

Results of the present study revealed that there was no marked influence of the cropping pattern in altering the performance, phenotypic and genotypic coefficients of variability, genetic parameters, correlation coefficients, and direct and indirect effects of seed technological traits.

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1) Recent advances in mutation-breeding research in soybean in India.

In spite of high yielding ability of Birsa Soybean-1 for the plateau region of Bihar, it has not become popular among the farmers because of its black seed-coat color. The seeds of Birsa Soybean-1 were irradiated with different doses of gamma rays at FCI Sindri, Bihar (India) in 1979. Progenies of a yellow-seeded 50 Kr. M-2 plant in M-3 gave very promising and interesting plant types (Prakash et al., 1984). Prakash et al. (1984) reported the change in color of Birsa Soybean-1 from black to yellow, dull brown, and brown.

Thirty stable lines having yellow, white, and brown seeds were evaluated in the rainy season of 1985-86 in randomized block design along with 4 checks. Each line was in three rows. Row-to-row distance was 45 cm and plant-to-plant distance was 8 cm. The results are presented in Table 1. As can be seen from the table, several strains gave superior yield in comparison with Birsa Soybean-1. It is hoped that further evaluation of these lines will result in isolating a superior genotype in comparison with Birsa Soybean-1.

Reference

Prakash, R., H. B. P. Trivedi, V. Kerketta and Md. F. Haque. 1984. Mutation breeding research in soybean in India. Soybean Genet. Newsl. 11:43-44.

Table 1. Performance of mutants of Birsa Soybean-1

S.N.	Variety/ strain	Height (cm)	No. pods	Days to maturity	100- seed weight (g)	Grain yield (q/ha)	Seed-coat color
1	43-2A	72.60	62.20	110.66	14.43	31.59	Brown
2	71-4B	58.33	61.20	108.00	11.63	27.39	Shining black
3	39-2B	60.46	48.66	112.00	15.76	27.04	Light brown
4	43-3A	61.26	54.60	105.00	12.73	25.91	Deep brown
5	39-8B	57.46	51.53	106.00	16.00	25.66	Brown
6	39-5B	55.13	48.26	107.66	14.80	25.42	Deep brown
7	51-4C	70.53	80.60	107.33	13.33	25.41	Brown
8	75-5B	65.60	68.53	107.66	13.03	25.17	Light brown
9	Bragg(c)	66.80	76.86	111.00	15.70	24.92	Yellow
10	9-5B	66.00	67.66	108.33	15.46	24.67	Light brown
11	44-7B	69.20	68.13	107.66	13.10	24.43	Deep brown
12	Birsa-Soy-1 (c)	60.90	80.70	104.33	13.26	24.43	Black
13	60-3A	111.20	57.46	108.66	12.33	23.69	Black
14	44-18B	75.93	67.66	106.33	13.50	23.44	Light brown
15	35-18B	85.86	73.66	108.33	11.53	23.19	Whitish yellow
16	PK-416(c)	57.60	51.93	107.00	14.73	22.95	Yellowing white
17	7-1B	81.93	90.53	107.66	12.36	22.70	Whitish yellow
18	68-7C	91.13	67.66	114.00	12.40	22.45	Whitish
19	41-11B	74.13	74.60	108.00	14.26	22.33	Deep brown
20	25-6B	98.33	109.80	112.66	12.50	22.12	Light yellow
21	68-7B	103.33	55.50	114.00	12.66	21.47	Whitish yellow
22	44-3B	84.93	71.66	110.33	12.43	21.46	Light brown
23	35-10B	86.66	95.20	108.33	12.46	21.22	Light white
24	65-5B	62.80	59.26	107.00	11.80	20.48	Whitish yellow
25	62-2B	97.00	59.00	107.00	15.40	20.23	Black
26	5-2B	66.00	88.06	113.00	14.03	20.23	Light brown
27	35-8B	83.26	110.60	107.33	9.93	19.74	Whitish
28	35-5B	68.40	48.26	112.00	10.93	19.74	Whitish yellow
29	35-4A	47.66	75.26	107.00	12.63	19.49	Whitish yellow
30	46-5B	91.66	63.13	107.66	13.23	18.75	Light brown
31	1-3B	62.90	83.06	107.66	12.33	18.75	White
32	2-2B	71.86	84.53	107.66	11.20	17.27	Whitish yellow
33	70-4B	46.33	79.86	106.33	11.16	14.80	Yellowish white
34	67-3B	58.86	84.06	107.33	14.66	11.38	Yellowish white
			C.V.	14.434 ha.			
			C.D. %	5.283			

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1) ²⁴⁵ Path-coefficient analysis of developmental and yield components in soybean.

Abstract: Interrelationships among different characters were determined by simple correlations and path-coefficient analysis using 36 diverse and elite cultivars representing different geographical origin. The results revealed a highly significant positive association of the branches per plant and pods per plant with grain yield. The pods per plant also showed a high direct influence on grain yield. Thus, from this investigation, it is suggested that pods per plant and number of branches per plant are the primary yield components that should be given due emphasis in selecting high yielding genotypes in soybean.

Introduction: Grain yield is a complex character and is the ultimate expression of different components. The knowledge of interrelationship among various developmental and productive traits is necessary for framing effective breeding programs. Further, path-coefficient analysis is useful in assessing the real contribution of various component characters towards grain yield, so that direction for desired improvement may be developed. Present study was undertaken to work out the association among various metric traits in soybean and to develop suitable selection criteria.

Materials and methods: Materials used and methods adopted for the present investigation have been described earlier (Rajput et al., 1985). However, the details are given below.

The experiment was conducted during summer 1984 at the AEARC, Experimental Farm, Tandojam. Thirty-six soybean varieties of diverse origin were grown in a randomized complete block design with four replications. Each replication consisted of a single 4-meter row. Seed was drilled at a row distance of 45 cm. Plant-to-plant distance was maintained at 5 cm by thinning the crop before first irrigation. At maturity, five competitive plants from each replication of all the varieties were randomly selected and observed for plant height, number of branches per plant, pod length, pods per plant, seeds per pod, 100-grain weight, and grain yield per plant.

The genotypic correlations were worked out according to the methods suggested by Hayes et al. (1955). Path-coefficient analysis was carried out according to the procedure outlined by Dewey and Lu (1959).

Results and discussion: All the characters have shown positive relationship with yield. Highly significant ($P > 0.01$) and positive correlation values between yield and pods per plant (0.8311) and branches per plant (0.6846) were observed (Table 1). Similar correlations have been reported earlier by Malhotra et al. (1972) and Lal and Haque (1971) in soybean. Estimates of correlations for plant height (0.3965) and pod length (0.3174) with grain yield were moderate but did not reach the significance level. Earlier, Giriraj and Kumar (1974) observed similar relationship between plant height and yield in mungbean.

Table 1. Correlation coefficients among different characters in soybean

Characters	Plant height	Pod length	Seeds/pod	Branches/plant	Pods/plant	100-grain weight	Grain yield
Plant height		-0.1775	0.0325	0.1731	0.4738*	-0.3819	0.3965
Pod length			0.6034**	0.1407	0.0341	0.3805	0.3174
Seeds/pod				-0.139	-0.0638	0.0924	0.1495
Branches/plant					0.7778**	-0.2444	0.6846**
Pods/plant						-0.3635	0.8312**
100-grain weight							0.0016

*,**Significant at the 5% and 1% levels, respectively.

The correlation values of six quantitative traits with grain yield are partitioned into direct and indirect effects (Table 2). These effects are also explained diagrammatically in Figure 1. Pods per plant registered the highest direct and positive effects (0.7833). 100-grain weight also exerted considerably high direct positive effect (0.3229). Direct effects of other characters like plant height, pod length, and seeds per pod were low, so did not appear to have influenced the grain yield substantially.

Pods per plant, which had registered maximum direct effect, also contributed to yield indirectly through branches per plant. Other traits like plant height and pod length also contributed via pods per plant to grain yield. This clearly establishes that pods per plant is the most important component of seed yield in soybean. Like the results of this investigation, Chand et al. (1957) and Katiyar et al. (1977) had earlier noted quite a large direct effect of pods per plant on seed yield and suggested that, while

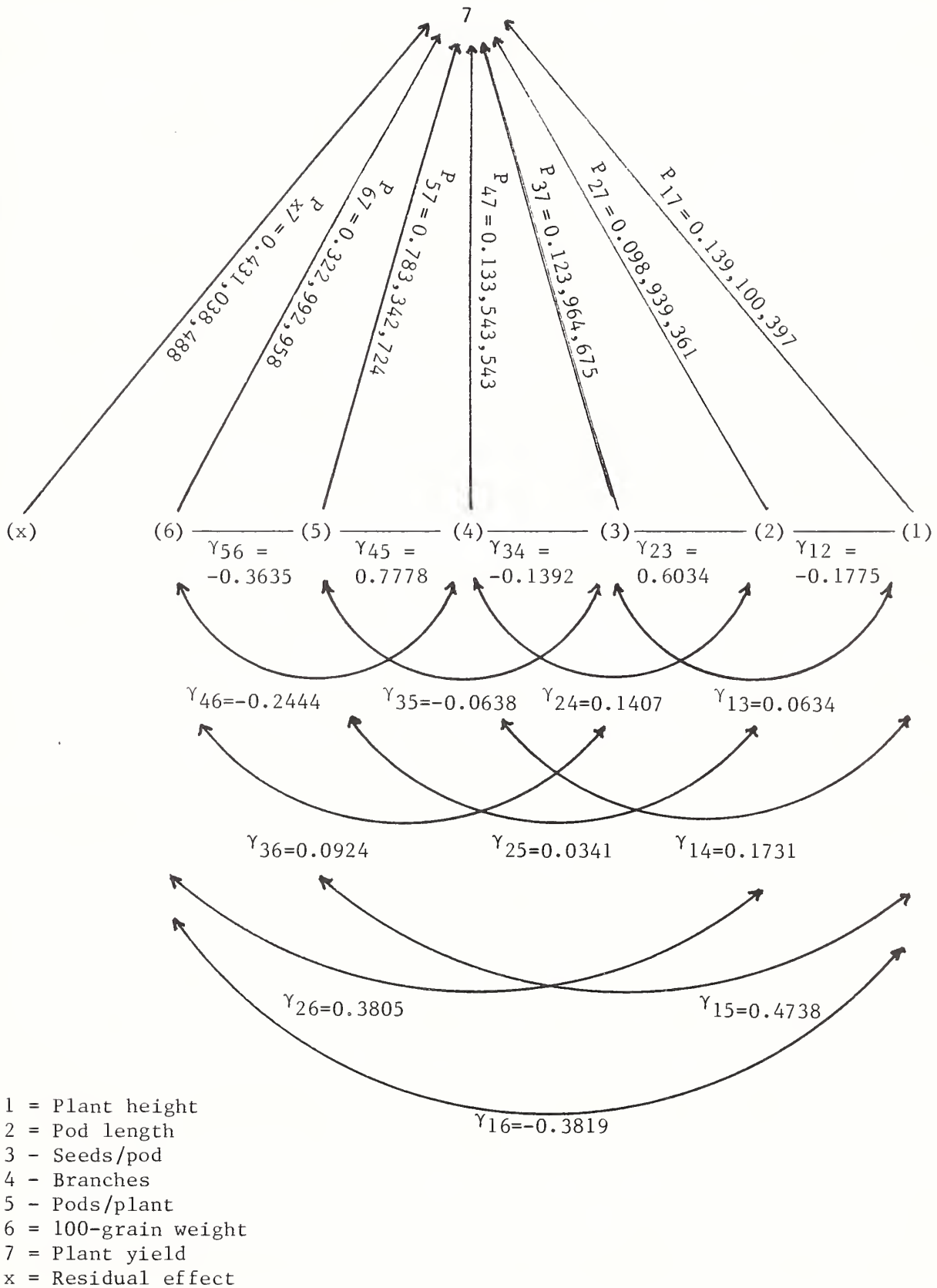


Fig. 1. Path diagram showing direct and indirect effects of various agronomic characters on grain yield in soybean

Table 2. Direct and indirect effects of different characters on grain yield in soybean

Characters	Plant height	Pod length	Seeds/pod	Branches/plant	Pods/plant	100-grain weight	Grain yield
Plant height	(0.1391)	-0.0175	0.0040	0.0231	0.3712	-0.1233	0.3964
Pod length	-0.0247	(0.0989)	0.0748	0.0188	0.0267	0.1229	0.3174
Seeds/pod	0.0045	0.0597	(0.1239)	-0.0186	-0.0499	0.0298	0.1495
Branches/plant	0.0241	0.0139	-0.0173	(0.1335)	0.6093	-0.0789	0.6846
Pods/plant	0.0659	0.0034	-0.0079	0.1039	(0.7833)	-0.1174	0.8312
100-grain weight	-0.0531	0.0376	0.0115	-0.0326	-0.2847	(0.3229)	0.0016

*Figures in parenthesis indicate direct effect.

selecting for high yield, main emphasis should be placed on pods per plant.

Branches per plant, another important component of yield as revealed by the present study, though having low direct effect, exerted high indirect effect via pods per plant making the total effect (0.6846) highly significant ($P > 0.01$). Similar findings have been reported earlier by Singh et al. (1977) in lentil.

The high value of the residual effect (0.431) was perhaps due to sampling error and many other characters that were not taken into consideration in the present study. From the foregoing discussion of the results obtained in the present study, it could be inferred that the pods per plant was the most important component of grain yield. Branches per plant was the other important component of yield in soybean. Thus, it is suggested that soybean ideotype for grain yield should be heavy bearing with profuse branching.

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1) Interdependences between some traits in early hybrid generations (F_2 - F_4) of soybean.

The existence of an interdependence between some important traits of soybean is of great significance for its breeding.

In rather cool climate (Poland) interdependences between developmental traits and yield structure elements affect the possibility of fast creation and introduction of new, well-adapted and efficient cultivars into agricultural practice.

Estimation of phenotypic correlations of 11 traits was the subject of this paper.

Materials and methods: Field experiments were carried out in 1979-81. Plants of six cross combinations in early (F_2 - F_4) respective generations were examined. Particular correlation coefficients were computed on the basis of the number of plants from 122 to 3770, according to combination and generation. Phenotypic correlation coefficients were computed for all combinations of pairs of the 11 traits mentioned below.

1. Period from sowing to beginning of flowering,
2. Flowering period,
3. Pod-filling period,
4. Vegetation period,
5. Plant height,
6. Number of branches per plant.
7. Number of pods per plant,
8. Number of seeds per plant,
9. Number of seeds per pod,
10. Weight of seeds per plant,
11. 100-seed weight.

This allowed us to evaluate 55 correlations of various pairs of these traits in examined populations. Correlation coefficients were computed individually for separate cross combinations and respective generations.

Results and comments: Among 55 estimated correlations between pairs of separate traits, only in 20 cases were coefficients meaningfully constant and essential in most of the investigated cross combinations and respective

generations. Only these 20 cases are taken into consideration in this article (Table 1).

The correlation between the period from sowing to flowering and the flowering period was not close but in most cases rather negative. Also, the flowering time was negatively correlated with the pod-filling period, and in this case correlation coefficients were slightly greater than in the former interdependence. These two correlations indicate that selection for short flowering time can result in extending the period from sowing to flowering and/or pod-filling period.

The period from sowing to flowering was positively correlated with plant height. This indicates that selection for higher plants can bring about a delay of beginning of flowering.

The pod-filling period was highly correlated with vegetation period and 100-seed weight. The vegetation period was positively correlated with plant height and weight of 100 seeds. These four correlations indicate that selection for earliness, height of plant, and large seeds in our conditions can be very difficult and requires searching for ways to break these unfavorable interdependences.

Morphological traits such as plant height and number of branches per plant were positively correlated with the number of pods and seeds per plant, as well as with seeds per pod and individual seed yield. These correlations show that selection for higher and more bushy plant types can be effective in yield potential. Among yield structure elements, rather high and positive interdependences were observed. Negative, consistent, but inconsiderable, correlation was observed only between the number of seeds per pod and weight of 100 seeds. Positive, rather close and consistent relationships between most of yield structure elements allows the breeders to reduce the number of traits taken into consideration, when they intend to select soybean for yield potential alone.

Discussion: Other researchers have dealt with interdependences between yield and other traits in soybean. Many investigators searched for traits that would be highly correlated with seed potential. Discovery of such trait (or traits) can improve selection for yield, which shows a rather small heritability coefficient in comparison with other characters. To find traits that would constitute good indicators of yield potential still is a very difficult task. Johnson and Bernard (1963) found that, in north latitude conditions, the great difficulty in soybean selection was presented by negative correlation

Table 1. Phenotypic correlation coefficients

Trait	Generation	Cross combination					
		PI 238920 x Oyachi No. 2	PI 238920 x PI 180509	PI 238920 x PI 180517	PI 248405 x Nordia-1	PI 248405 x PI 194643	Fiskeby V x PI 180502
Period from sowing to flowering							
Flowering period	2	-0.40**	0.27**	-0.13**	-0.04	-0.01	0.17**
	3	-0.51**	-0.08	-0.02	-0.25**	-0.36**	-0.03
	4	-0.02	-0.03	-0.18	-0.03	-0.04	
Plant height	2	0.27**	0.24**	0.05	0.32**	0.59**	0.30**
	3	0.11	0.12	0.17**	0.29**	0.31**	0.44**
	4	0.45**	0.12	0.01	0.36**	0.06	
Flowering period							
Pod-filling period	2	-0.15	-0.32**	-0.33**	-0.59**	-0.62**	-0.62**
	3	-0.15	-0.28**	-0.27**	-0.81**	-0.52**	-0.64**
	4	-0.27**	-0.48**	-0.21*	-0.43**	-0.39**	
Pod-filling period							
Vegetation period	2	0.90**	0.82**	0.77**	0.47**	0.42**	0.70**
	3	0.57**	0.90**	0.89**	0.24**	0.60**	0.41**
	4	0.65**	0.61**	0.80**	0.62**	0.56**	
100-seed weight	2	0.47**	0.28**	0.26**	0.36**	0.29**	0.19**
	3	0.18	0.50**	0.36**	0.08	0.36**	0.15**
	4	0.10	0.24**	0.47**	0.41**	0.10	
Vegetation period							
Plant height	2	0.36**	0.33**	0.19**	0.53**	0.59**	0.49**
	3	0.43**	0.52**	0.59**	0.43**	0.16**	0.60**
	4	0.49**	0.49**	0.64**	0.65**	0.58**	
100-seed weight	2	0.51**	0.38**	0.36**	0.47**	0.34**	-0.04
	3	0.32**	0.55**	0.39**	0.13	0.41**	-0.09
	4	0.03	0.23**	0.52**	0.26**	0.09	

Table 1. Continued

Trait	Generation	Cross combination					
		PI 238920 x Oyachi No. 2	PI 238920 x PI 280509	PI 238920 x PI 180517	PI 248405 x Nordia-1	PI 248405 x PI 194643	Fiskeby V x PI 180502
Plant height							
Pod number	2	0.17*	0.38**	0.41**	0.18*	0.33**	0.53**
per plant	3	0.27**	0.24**	0.14**	0.07	0.39**	0.22**
	4	0.14	0.07	0.42**	0.13	0.29*	
Seed number	2	0.12	0.31**	0.38**	0.15	0.31**	0.57**
per plant	3	0.29**	0.29**	0.22**	0.03	0.43**	0.25**
	4	0.07	0.06	0.31**	0.24	0.32*	
Seed weight	2	0.19*	0.35**	0.42**	0.21*	0.32**	0.53**
per plant	3	0.34**	0.39**	0.33**	0.18*	0.40**	0.14**
	4	0.06	0.13	0.44**	0.24	0.20	
Number of branches per plant							
Pod number	2	0.50**	0.58**	0.61**	0.59**	0.62**	0.63**
per plant	3	0.42**	0.34**	0.46**	0.37**	0.49**	0.26**
	4	0.67**	0.54**	0.43**	0.37**	0.39**	
Seed number	2	0.51**	0.53**	0.57**	0.57**	0.61**	0.66**
per plant	3	0.39**	0.33**	0.46**	0.40**	0.53**	0.13**
	4	0.28**	0.42**	0.39**	0.17**	0.38**	
Seed weight	2	0.52**	0.53**	0.53**	0.58**	0.57**	0.61**
per plant	3	0.36**	0.29**	0.43**	0.32**	0.39**	0.23**
	4	0.30**	0.48**	0.31**	0.27**	0.15	

Table 1. Continued

Trait	Generation	Cross combination					
		PI 238920 x Oyachi No. 2	PI 238920 x PI 280509	PI 238920 x PI 180517	PI 248405 x Nordia-1	PI 248405 x PI 194643	Fiskeby V x PI 180502
Pod number per plant							
Seed number	2	0.95**	0.96**	0.97**	0.98**	0.97**	0.95**
per plant	3	0.95**	0.93**	0.93**	0.91**	0.95**	0.84**
	4	0.65**	0.86**	0.91**	0.77**	0.80**	
Seed weight	2	0.92**	0.95**	0.95**	0.95**	0.95**	0.92**
per plant	3	0.93**	0.85**	0.88**	0.80**	0.92**	0.80**
	4	0.64**	0.74**	0.85**	0.73**	0.62**	
Seed number per plant							
Seed number	2	0.57**	0.36**	0.44**	0.19*	0.23**	0.52**
per pod	3	0.49**	0.56**	0.44**	0.30**	0.42**	0.53**
	4	0.57**	0.35**	0.33**	0.33**	0.50**	
Seed weight	2	0.94**	0.96**	0.97**	0.97**	0.96**	0.96**
per plant	3	0.95**	0.91**	0.93**	0.87**	0.93**	0.90**
	4	0.84**	0.78**	0.88**	0.81**	0.77**	
Seed number per pod							
Seed weight	2	0.44**	0.29**	0.37**	0.13	0.13	0.48**
per plant	3	0.36**	0.48**	0.40**	0.26**	0.30**	0.42**
	4	0.57**	0.14	0.27**	0.15	0.36**	
100-seed	2	-0.24**	-0.21**	-0.12	-0.35**	-0.12	-0.21**
weight	3	-0.03	-0.22**	-0.04	-0.11	-0.25**	-0.26**
	4	-0.15	-0.39**	-0.10	-0.20	-0.03	
Seed weight per plant							
100-seed	2	0.33**	0.31**	0.35**	0.39**	0.28**	0.03
weight	3	0.38**	0.53**	0.30**	0.28**	0.20**	0.20**
	4	0.06	0.37**	0.50**	0.45**	0.56**	

*Significant level 0.05.

**Significant level 0.01.

between early maturity and plant height as well as by a positive correlation of plant height and seed yield. Our investigations corroborated these interdependences in all analyzed cross combinations and generations. Skorupska and Konieczny (1985) found in an experiment with two cross combinations (F_4) correlation values for earliness and plant height equal -0.45 and -0.20 , for earliness and seed weight per plant -0.64 and 0.09 , and for the same two crosses in F_3 and F_4 generations for plant height and seed yield per plant in F_3 -0.34 ; 0.22 , and in F_4 0.30 and -0.23 , respectively, for cross "A" and "B". According to Fedorowska (1981), the value of correlation coefficient between plant height and vegetation period was 0.21 . The present investigations produced significantly greater value of this coefficient (Table 1). In our conditions, direct interdependence between the vegetation period and seed yield per plant was small, insignificant, and variable. Such creation of the latter interdependence in hybrid plants ($F_2 - F_4$) allows us to state that selection for early forms with satisfactory yield potential in spite of great difficulties can bring expected results.

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2) ²⁴⁵ Performance of some important characters of hybrid soybean (F₁) in a cool climate.

Obtaining intervarietal hybrids of *Glycine max* (L.) Merrill in a cool climate such as in Poland (latitude above 50°N) is one of the most important problems for development and introduction of original cultivars of this species.

In 1977, hybrid soybean seeds were obtained for the first time in our Academy through field crossing of various forms (cultivars and PI's). Characteristics of some important traits of F₁ plants in comparison with their parental forms were the subject of this paper.

Materials and methods: This study presents characteristics of F₁ individuals and their parental forms in Wielkopolska region (latitude 51-53°N).

Cross components and their characteristics for a three-year period in Polish conditions are presented in Table 1.

Table 1. Characteristic of parental forms from three-year observations (1975-77)

Cultivar or PI	Vegetation period (days)	Plant height (cm)	Seed weight per plant (g)	Seed number plant	100-seed weight (g)
Fiskeby V	124	29.0	6.5	34.0	19.5
Nordia-1	136	58.7	10.4	58.0	18.6
Oyachi No. 2	164	61.0	6.3	24.0	21.4
Merit	176	78.0	8.9	61.0	14.6
PI 180499	166	82.0	15.0	80.0	18.7
PI 180502	160	84.0	11.7	68.0	18.0
PI 180509	142	63.0	12.7	69.0	17.4
PI 180517	143	68.0	11.2	62.0	17.7
PI 194643	130	52.0	8.1	40.0	18.7
PI 238920	135	58.0	7.2	39.0	18.9
PI 248405	150	60.0	8.0	42.0	19.6
PI 297503	169	64.0	14.0	78.0	18.7

Seeds of the F₁ generation were planted on April 27, 1978, in the field of Experimental Station at Swadzim. Distances between rows were 0.5 m, and interplant space in rows was 0.4 m. Parental forms were planted in the same

Table 2. Characteristic of F₁ plants in comparison with their parental forms in 1978

Combination	Number of plants	Number of days				Plant height (cm)
		from sowing to flowering	of flowering	of pod filling	of vegetation	
Oyachi No. 2 x PI 238920	2	74	26	73	173	59.5
PI 238920 x Oyachi No. 2	1	71	29	84	184	65.0
PI 238920 x Merit	1	92	26	64	186	120.0
PI 238920 x PI 180499	2	78	52	56	186	97.0
PI 238920 x PI 180509	4	84	47	42	173	59.0
PI 238920 x PI 180517	3	82	20	69	171	53.7
PI 238920 x PI 297503	1	77	54	55	186	95.0
PI 248405 x Nordia-1	2	69	30	71	170	73.0
PI 297503 x PI 238920	2	83	35	68	186	86.6
PI 248405 x PI 194643	5	68	39	66	173	86.2
Fiskeby V x PI 180502	3	57	35	51	143	82.7
Fiskeby V	10	46	13	54	113	42.6
Nordia-1	10	64	40	66	170	60.2
Oyachi No. 2	10	74	26	73	173	64.0
Merit	10	84	34	67	185	75.8
PI 180499	10	66	52	67	185	78.3
PI 180509	10	85	33	67	185	63.1
PI 180507	10	85	19	66	170	45.8
PI 194643	10	61	39	70	170	66.0
PI 180502	10	60	69	39	168	86.2
PI 238920	10	73	27	73	173	58.0
PI 248405	10	66	30	77	173	50.1
PI 297503	10	66	44	75	185	66.5

Number of				Weight of	
branches per plant	Pods per plant	seeds per plant	seeds per pod	seeds per plant (g)	100 seeds (g)
7.0	61.5	88.0	1.4	19.0	21.6
7.0	31.0	40.0	1.3	9.5	23.6
10.0	30.0	31.0	1.0	3.0	9.7
8.0	22.5	32.0	1.4	4.0	12.5
5.8	55.0	68.2	1.2	12.9	18.7
6.7	75.7	98.3	1.3	18.5	18.8
9.0	12.0	4.0	0.3	0.5	12.5
6.0	74.5	102.0	1.4	17.3	16.9
6.8	13.2	8.5	0.6	1.1	12.8
5.2	35.6	57.8	1.6	11.5	19.9
10.3	117.7	221.0	1.9	42.1	19.0
5.0	67.4	130.4	1.9	22.6	17.3
3.2	26.9	34.4	1.3	4.6	13.2
4.5	17.3	24.2	1.4	6.7	27.7
4.3	26.3	35.5	1.4	3.0	8.5
3.0	13.7	21.0	1.5	2.8	13.2
5.3	21.3	28.3	1.3	4.2	15.1
5.0	32.7	51.3	1.6	6.8	13.3
5.5	21.2	30.1	1.4	3.9	12.9
8.2	50.2	93.2	1.8	23.5	25.2
4.1	17.5	20.9	1.2	3.5	16.8
3.1	21.9	31.3	1.4	4.1	13.0
5.2	18.5	21.3	1.2	1.8	8.6

Table 3. Relative value of morphological and yield structure traits of F_1 plants in comparison with their maternal (P_1) and paternal (P_2) forms, in percent

Combination	Number of					
	Plant height		Branches per plant		Pods per plant	
	P_1	P_2	P_1	P_2	P_1	P_2
Oyachi No 2 x PI 238920	93.0	102.6	155.5*	155.5*	355.5	351.4*
PI 238920 x Oyachi No. 2	112.0	101.6	155.5*	155.5*	177.1*	179.2
PI 238920 x Merit	206.9	158.3*	222.2*	232.5	171.4	114.1*
PI 238920 x PI 180499	167.2	123.9*	177.8*	266.7	128.6*	164.2
PI 238920 x PI 180509	101.7	93.5	128.9	109.4*	314.3	258.2*
PI 238920 x PI 180517	92.6	117.2	148.9	134.0*	432.6	231.5*
PI 238920 x PI 297503	163.8	142.8*	200.0	173.1*	68.6	64.9
PI 297503 x PI 238920	130.2*	149.3	130.8*	151.1	73.1	75.4
PI 248405 x Nordia-1	145.7	121.3*	193.5	187.5*	340.2	276.9*
PI 248405 x PI 194643	172.0	130.6*	167.7	94.5	162.5*	168.7
Fiskeby V x PI 180502	194.1	95.9	206.0	125.6*	174.6*	234.4

*Relative trait value in which heterosis vigor was noted in comparison with more efficient parental form.

Number of —————				————— Weight of —————			
Seeds per plant		Seeds per pod		Seeds per plant		100 seed	
P ₁	P ₂	P ₁	P ₂	P ₁	P ₂	P ₁	P ₂
363.6*	421.0	100.0	116.7	283.6*	542.8	78.0	128.7
191.4	165.3*	108.3	93.0	271.4	141.8*	141.6	85.8
148.3	87.3	83.3	71.4	85.7	100.0	57.6	114.4
153.1	152.4*	116.7	93.3	114.3*	142.8	74.5	94.9
326.3	243.6	100.0	92.3	368.6	307.1*	111.3*	124.0
470.3	191.6*	108.3	81.2	528.6	272.0*	112.2*	141.3
19.1	18.8	25.0	25.0	14.3	27.8	74.5	145.5
39.9	40.7	50.0	50.0	61.1	31.4	148.9	99.4
325.9	296.5*	100.0	107.7	421.9	376.1*	130.1	127.9
184.7*	193.0	114.3*	114.3*	280.5*	294.9	152.8*	154.4
169.5*	237.1	100.0	105.5	186.3	179.1*	109.8	75.4

pattern next to F_1 plants. Some phenological traits (flowering and maturity), morphological traits (plant height, number of branches per plant), and yield structure elements (number of pods and seeds per plant, number of seeds per pod, weight of a hundred seeds) were observed.

Results: *Phenological characters.* F_1 plants and their parental forms emerged between the 12th and 14th of May. The emergence of the above forms was not observed earlier than that. In analyzed populations of F_1 plants, the earliest blooming was observed in plants of the cross Fiskeby V x PI 180502 - 57 days after planting (Table 2). Parental forms of this cross started to flower after 46 and 60 days from sowing, respectively. The shortest period of flowering (only 20 days) was observed in cross PI 238920 x PI 180517, in which parental forms flowered for 27 and 19 days, respectively. The period of pod filling varied. The shortest one was observed in F_1 plants from PI 238920 x PI 180509 combination in which it was 42 days only. Pod-filling period for parental forms was 73 and 67 days, respectively. Plants from particular cross combinations were characterized by different vegetation periods. The shortest one was observed in F_1 plants of Fiskeby V x PI 180502 -- only 143 days -- and was intermediate in comparison with their parental forms, which vegetated 113 and 168 days, respectively. Phenological traits are important qualities, especially in long day conditions. Breeders are looking for plants that start to flower early and flower not too long, are rather thermoneutral and photoperiodneutral and also usually mature early.

Morphological characters. Plants in 6 of 11 observed cross combinations were taller than both their parents (Tables 2 and 3). In cross PI 238920 x PI 180517, F_1 plants were intermediate in comparison with their parental forms. In 10 combinations, F_1 plants produced more branches than their parental forms (Tables 2 and 3).

Yield structure elements. Observations of the number of pods and seeds per plant and weight of seeds per plant indicated that most F_1 plants were distinctively more productive than their efficient parental forms. Plants in the analyzed population, regarding the number of seeds per pod, were not so much differentiated as regarding the characters mentioned above. Weight of 100 seeds was differentiated according to the particular crosses. F_1 plants from crosses PI 248405 x PI 194643, PI 248405 x Nordia-1, PI 238920 x PI 180509, and PI 238920 x PI 180517 produced larger seeds than parental forms with heavier seeds (Tables 2 and 3).

Discussion: Jaranowski et al. (1980) reported that foreign soybean genotypes obtained in similar latitude as in Poland (the same daylength) significantly prolonged their vegetative period in our conditions. Similar reaction was observed in Sweden by Holmberg (1973). For this reason, soybean breeders in Poland create a new original genetic variation by means of crossing different genotypes coming from various regions, especially of high north latitude. Some reports provide information about F_1 plant traits as compared with their parental forms. Kalton (1948), Leffel and Weiss (1958), Brim and Cockerham (1961), Chaudhary and Singh (1974), Paschal and Wilcox (1975), and Kunta et al. (1985) described the heterosis effect of several characters in F_1 plants. They found significant hybrid vigor but none of them reported F_1 plants characterized by so much better traits as compared with the more efficient parent in the experiment. For instance, in cross PI 248405 x Nordia-1, F_1 plants yielded 276.1% more (grams of seeds per plant) than their better parent. In the same cross, it was found that the number of seeds per plant exceeded the better parental form above 196.5%. Such distinct hybrid vigor in F_1 plants was probably due to poor environmental conditions for soybean growing in Poland.

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²⁴⁵
D. A spontaneous narrow-leaflet mutant

At the Asian Vegetable Research and Development Center, developing improved vegetable soybeans is one of the objectives. In accomplishing that objective, one of the crosses involved AGS 188, PI 157424 from Maturity Group IV and G 10381, cultivar 'Kaohsiung' No. 8 released by the Kaohsiung District Agricultural Improvement Station in Pingtung, Taiwan. The F_1 and F_2 progenies of the cross were normal. In the F_3 generation, some lines appeared with narrow leaflets and with virus-like symptoms. Some of the lines had broad-leaflet (length/width ratio 1:8 or less) plants as well as narrow-leaflet (length/width ratio 2:2 or greater) plants.

Seeds of the six broad-leaflet and two narrow-leaflet plants from different segregating lines were chosen at random and were progeny tested in F_4 . One line had only broad-leaflet plants and two lines had only narrow-leaflet plants. Five lines segregated for leaf types (Table 1a). Assuming that all those that segregated were derived from heterozygous plants, the data were pooled and the chi square was calculated. Segregation of each line also was analyzed separately. The pooled data had a chi square of 0.0186 with a P of 0.80 to 0.90, giving a good fit for 13:3 ratio. Individual chi-square test of each of the five segregating lines gave a good fit for 3:1 (2 lines), 13:3 (2 lines) and 15:1 (one line) (Table 1a).

Seeds from four narrow-leaflet plants and four broad-leaflet plants from F_3 also were planted in the greenhouse and observed for leaflet type. Six lines showed no segregation, of which four had narrow leaflets and two had broad leaflets. One line segregated with 8 normal broad leaflet to 2 narrow leaflet, which gave a good fit for 13:3 ratio with a P of 0.80 to 0.90 (Table 1b).

Based on the pedigree of the cross (Figure 1), it would appear that the narrow-leaflet trait arose as a spontaneous mutation in F_2 and was expressed in the F_3 generation, since there was no evidence of segregation in the F_2 generation. Furthermore, the parents used in the cross did not express the trait. Although the two parents were also involved as parents in a number of other crosses with other genotypes, narrow leaflet was not observed in any of the other combinations. With the available data, the identity of the narrow allele(s) cannot be unequivocally established.

Table 1a. Segregation in F₄ lines derived from randomly selected F₃ plants

F ₃ line no.	Phenotype in F ₃	Genotype Phenotype	Homozygous broad ^a	Heterozygous broad	Heterozygous narrow ^b	Homozygous narrow	χ^2 (ratio)	P
No. of plants								
GC 83005-1	Broad		25	0	0	0	2.173 (3:1)	0.10-0.20
GC 83005-6	Broad		0	19	11	0	1.111 (3:1)	0.20-0.30
GC 83005-16	Broad		0	20	10	0	1.867 (13:3)	0.20-0.30
GC 83005-17	Broad		0	25	3	0	0.8875 (13:3)	0.30-0.50
GC 83005-18	Broad		0	23	3	0		
GC 83005-43	Narrow		0	0	0	15		
GC 83005-49	Broad		0	46	3	0	0.0010 (15:1)	0.98-0.99
GC 83005-82	Narrow		0	0	0	14		
Heterozygous lines pooled			133	30			0.02265 (13:3)	0.80-0.90

Table 1b.

GC 83005-6	Broad	0	8	2	0	0.0103 (13:3)	0.80-0.90
GC 83005-6	Narrow	0	0	0	10		
GC 83005-16	Broad	10	0	0	0		
GC 83005-16	Narrow	0	0	0	10		
GC 83005-17	Broad	10	0	0	0		
GC 83005-17	Narrow	0	0	0	10		
GC 83005-21	Broad	10	0	0	0		
GC 83005-82	Narrow	0	0	0	10		

^aBroad leaflet.^bNarrow leaflet.

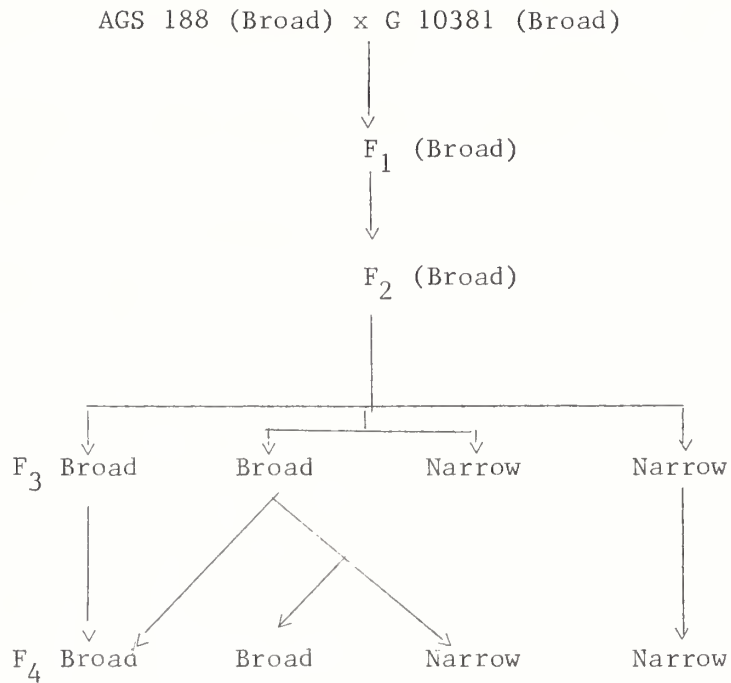


Figure 1. Origin and segregation of a narrow-leaflet mutant
(Broad = broad leaflet; Narrow = narrow leaflet)

The genetics of the narrow-leaflet mutant and its relationship to the 'ln' allele is currently being investigated.

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1) ⁹⁴⁵ Inheritance of metribuzin sensitivity in the soybean cultivar, 'Altona'.

Metribuzin [4-amino-6-tert-butyl-3-(methylthio)-as-triazin-5(4H)-one] is an herbicide that can be effective in controlling many broadleaf weeds in soybeans. However, some soybean cultivars are sensitive to metribuzin and can suffer considerable damage (Wax et al., 1976). Previous research has established that a single recessive gene, *hm*, conditions the sensitive reaction of 'Semmes' (Edwards et al., 1976) and 'Tracy' (Kilen and Barrentine, 1983) to metribuzin. The *hm* gene and the *Rps*₁^b gene for phytophthora root rot [caused by *Phytophthora megasperma* f. sp. *glycinea*] resistance are closely linked (Kilen and Barrentine, 1983). 'Altona', a cultivar of maturity group 00, has the *Rps*₆ gene for phytophthora root rot resistance (Athow and Laviolette, 1982) and is sensitive to metribuzin (Wax et al., 1976). The objective of this study was to examine the inheritance of metribuzin sensitivity in Altona, and to determine if that cultivar's sensitivity also is due to the *hm* gene.

Materials and methods. Altona, K74-104-76-167, 'Century', and 'Sprite' were used as parents in these experiments. K74-104-76-167 is a metribuzin-sensitive line selected from a cross between Tracy and 'Williams'; Century and Sprite are tolerant to metribuzin. Sprite and Altona were crossed to investigate the inheritance of Altona's sensitivity to metribuzin. K74-104-76-167 and Century were crossed to confirm the presence of the *hm* allele in K74-104-76-167. Segregating progeny of the cross between Altona and K74-104-76-167 were tested to determine if the same gene or different genes were responsible for their metribuzin-sensitivity. F₃ families were classified according to the reactions of five plants. Gene model hypotheses were tested by chi-square analysis.

The F₁ and F₂ plants, and the F₃ families were evaluated in hydroponics in the greenhouse by a technique similar to one developed by Barrentine et al. (1976). The seeds were germinated in sand after treatment with the fungicide, thiram. The seedlings were transferred from sand to a 1X modified Hoagland's solution (Crafts-Brandner and Harper, 1982) when the cotyledons were in the hook stage. The plants were inserted through 0.64 cm holes drilled through white, 1.9 cm thick styrofoam sheets enabling the roots to dangle in the nutrient solution. Brown, plastic dishpans 29.2 cm x 39.4 cm x 13.3 cm deep

served as containers for the solution. Each pan held 8 liters of solution for 35 plants, 5 plants of each parent and 25 of F_1 , F_2 , or F_3 .

When the plants grew unifoliolate leaves, the nutrient solution was discarded and replaced with fresh solution plus an aliquot of metribuzin at a rate of $150 \mu\text{g l}^{-1}$. Plants developed injury symptoms about three days after introduction of the metribuzin. Those plants which survived after plants of the metribuzin-sensitive parental line had died were judged tolerant to metribuzin; plants killed were classified as sensitive.

Results and discussion. Sprite and Century were tolerant to metribuzin and K74-104-76-167 and Altona were sensitive to metribuzin (Table 1). The one tolerant Altona plant may have been an escape, or a result of an impure seed supply; occasional metribuzin-tolerant plants have been noted in cultivars sensitive to metribuzin (Barrentine et al., 1979). The reactions of the F_2 population and F_3 families of the Sprite X Altona cross fit a single recessive gene inheritance model for metribuzin sensitivity in Altona.

The results of the F_3 family screening of the cross K74-104-76-167 X Century corroborate those of the F_2 plant screening; K74-104-76-167 has the *hm* gene from Tracy.

Although in the K74-104-76-167 X Altona cross, two tolerant plants in the F_2 and one segregating F_3 family were observed, it can be concluded that Altona and Tracy possess the same gene for metribuzin sensitivity (*hm*). Since the two tolerant F_2 plants were next to each other in the screening, there may have been an environmental factor which delayed their injury symptoms. The one segregating F_3 family may have been derived from a foreign F_2 seed or may have delayed injury. More segregating F_3 families should have been observed, possibly fitting a 1 tolerant: 8 segregating: 7 sensitive ratio, if two recessive genes were involved.

The *hm* gene causes metribuzin sensitivity in Altona and appears to be important in conditioning metribuzin sensitivity over a wide range of soybean maturity groups. The fact that metribuzin sensitivity is due to simple inheritance eases the task of eliminating sensitive soybean genotypes.

Table 1. Reactions of parents, F₁ and F₂ plants, and F₃ families to 150 µg l⁻¹ metribuzin in hydroponics

Cross	No. plants or families				Chi-square	Probability
	Tolerant	Segregating	Sensitive			
Sprite	40		0			
Century	40		0			
K74-104-76-167	0		40			
Altona	1		38			
Sprite X Altona (F ₁)	10		0			
Sprite X Altona (F ₂)	144		36		3:1	0.5-0.1
Sprite X Altona (F ₃)	10	19	14		1:2:1	0.9-0.5
K74-104-76-167 X Century (F ₁)	31		0			
K74-104-76-167 X Century (F ₂)	146		52		3:1	0.9-0.5
K74-104-76-167 X Century (F ₃)	11	20	11		1:2:1	0.9-0.5
K74-104-76-167 X Altona (F ₁)	0		13			
K74-104-76-167 X Altona (F ₂)	2		182			
K74-104-76-167 X Altona (F ₃)	0	1	39			

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 1) A greenhouse method of screening soybeans for resistance to *Fusarium* wilt.

Fusarium wilt of soybean (causal organism: *Fusarium oxysporum* Schlecht. emend. Snyder & Hans.) has become an increasingly severe disease in the breeding plots at Gainesville and may be an undiagnosed or misdiagnosed problem in soybean production fields. At Gainesville, severity of *Fusarium* wilt, or a complex which includes *F. oxysporum*, has reduced yields in some plots to nearly zero. However, resistance to the disease has been observed in the breeding material, particularly in the "vegetable type" families which have 'Late Giant' as a parent, and in other families to a lesser extent. Variability in symptom expression within and among families is confounded with differences in the inoculum levels encountered throughout the field. Diseased and dead plants occur in patches of irregular shape. This field variability hinders progress in the selection of resistant types. Additionally, interactions between *F. oxysporum* and other soybean pests, particularly nematodes, may further obscure accurate selection. A greenhouse screening method would greatly facilitate the selection of resistant types by reducing the effects of variability found in field nurseries. This report describes some results of our efforts to screen soybeans for resistance to *Fusarium* wilt in the greenhouse.

Materials and Methods: Samples of discolored vascular tissue from field-grown soybeans were surface sterilized with 0.5% NaOCl and plated on acid PDA (aPDA) and peptone PCNB agar. After 8 days, clean cultures were transferred to carnation leaf water agar and aPDA to induce sporulation and for identification. Positive colonies of *F. oxysporum* were mass transferred to aPDA and kept at 21°C in constant light for inoculum production. After 2 weeks, the plates were rinsed with sterile distilled water, the propagules collected, and the suspension adjusted to 6×10^4 propagules/ml with a hemacytometer. The propagule suspension was added to sterilized greenhouse mix and preliminary pathogenicity testing began. Reisolation from diseased plants confirmed pathogenicity of the isolate. Soil from the preliminary tests was sampled and assayed to determine the final concentration of *F. oxysporum* propagules by soil dilution plating on a selective medium described by Komada (1975).

Five soybean lines were used in this experiment: Late Giant, F80-6717, Co82-645, D78-4668, and 'Yelredo'. Late Giant is a black-seeded "vegetable

type" of uncertain origin that has shown resistance to *Fusarium* wilt in the field and the preliminary greenhouse tests. F80-6717 is a black-seeded breeding line that has Late Giant in its parentage. Co82-645 is a breeding line from CR SEEDS with resistance to soybean cyst (*Heterodera glycines*) race 3 (SCN) and root knot (*Meloidogyne incognita* and *M. arenaria*) (RKN) nematodes. D78-4668 is a breeding line supplied by E. E. Hartwig, Stoneville, MS, from which *F. oxysporum* has previously been isolated. Armstrong and Armstrong (1950) have reported Yelredo to be very susceptible to *Fusarium* wilt.

Test design was a Latin Square with one square for each of three inoculum levels. Undiluted, infested soil from the preliminary tests was used as the base level of inoculum (13500 propagules/g soil). Samples of this soil were diluted with unsterilized greenhouse mix to levels of 10% and 5% of the base level. Six seeds of each soybean line were planted 2.5 cm deep in 15 cm plastic pots in the greenhouse and thinned at 7 days to three uniform plants/pot. One pot of each line was planted in unsterilized greenhouse mix as controls. Temperature and humidity were not controlled, but were within the range that permitted rapid plant development. Visual ratings were made weekly beginning 14 days after planting and ending 35 days after planting. Ratings were on a 1 to 5 scale with 1 equal to the noninoculated control, intermediate scores reflecting increasing chlorosis, and 5 indicating severe necrosis, particularly of the expanding trifoliolates.

Results and Discussion: Mean scores for 14 and 35 days from planting were not significantly different for any of the three inoculum levels. Mean scores for reaction of the five lines to the three levels of *F. oxysporum* at 21 and 28 days from planting are presented in Table 1.

The best separation of mean scores for all lines was obtained 21 days after planting in soil containing 1350 propagules/g soil. This was also the combination with the largest difference between the highest and lowest mean scores. Late Giant consistently had the lowest, or equal to the lowest, mean scores. D78-4668 was scored significantly more susceptible than Late Giant only at 21 days from planting and 1350 propagules/g soil. F80-6717 received significantly more susceptible scores than Late Giant only at the 1350 propagules/g soil inoculum level at both 21 and 28 days from planting, and only at 21 days from planting could F80-6717 be distinguished from the susceptible check, Yelredo. Thus, F80-6717 probably did not receive the full gene complement for resistance from Late Giant.

Table 1. Mean score of soybean lines grown in greenhouse soil infested with *Fusarium oxysporum*

Line	21 days from planting			28 days from planting		
	— Propagules/g soil —			— Propagules/g soil —		
	13500	1350	675	13500	1350	675
	Score ⁺					
Late Giant	2.6 a	2.0 a	1.0 a	3.6 a	3.2 a	1.8 a
D78-4668	3.2 ab	2.6 b	1.0 a	4.0 ab	3.2 a	2.0 a
F80-6717	3.2 ab	3.0 bc	1.0 a	4.2 ab	4.0 b	2.4 a
Co82-645	3.4 b	3.4 cd	1.6 b	4.4 b	4.0 b	2.4 a
Yelredo	3.8 b	3.6 d	1.2 ab	4.6 b	4.0 b	2.2 a

⁺From 1 = noninoculated control to 5 = severe. Means in columns followed by the same letter not significantly different at 5% level based on Duncan's New Multiple Range Test.

Co82-645 was scored significantly more susceptible than Late Giant in all but one combination of reading date and inoculum level (28 days from planting and 675 propagules/g soil). Ross (1965) has shown a detrimental interaction of *F. oxysporum* and SCN or RKN versus a weakly pathogenic reaction of *F. oxysporum* on nematode-susceptible soybeans in the absence of nematodes. In a soil assay performed after completion of this study, no nematodes were found in the infested soil. The severe damage from *F. oxysporum* occurred independently of nematodes on both nematode-susceptible and -resistant soybeans.

The susceptibility of Yelredo to Fusarium wilt was confirmed. On both reading dates, at 13500 and 1350 propagules/g soil, Yelredo had the highest, or equal to the highest, mean scores of all lines tested.

Using this greenhouse method, we were able to reliably separate resistant and susceptible soybean lines. Additionally, the short screening duration provides rapid determinations of reaction. With modifications, this method could prove useful in inheritance and other genetic studies. Further testing is in progress to identify better adapted sources of resistance, develop a nonsubjective scoring technique, and modify the method to allow more detailed evaluations.

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- 1) ²⁴⁵ Genes for resistance to *Phytophthora megasperma* f. sp. *glycinea* in PI 273483D, PI 64747, PI 274212, PI 82312N, and PI 340046.

Several years ago, we identified seven plant introductions resistant to the 16 races of *Phytophthora megasperma* f. sp. *glycinea* Kuan and Erwin (Pmg) known at that time. Each of these was crossed to the eight cultivars in Table 1 to determine how resistance was controlled. They were not crossed to cultivars that contained *Rps*₂ or *Rps*₅ because *Rps*₂ was found using root inoculation in a liquid culture solution, and *Rps*₅ was described after this study was started.

Table 1. Cultivars used in crosses and their gene(s) for resistance and reaction to physiologic races 1 through 9 of *P. megasperma* f. sp. *glycinea*

Cultivar	Gene(s)	Reaction to physiologic race ^a								
		1	2	3	4	5	6	7	8	9
Harosoy	<i>rps</i>	S	S	S	S	S	S	S	S	S
Mukden	<i>Rps</i> ₁	R	R	S	S	S	S	S	S	S
Sanga	<i>Rps</i> ₁ ^b	R	S	R	R	R	R	R	R	R
Wells II	<i>Rps</i> ₁ ^c	R	R	R	S	S	R	R	R	R
Williams 82	<i>Rps</i> ₁ ^k	R	R	R	R	R	R	R	R	R
PI 86972-1	<i>Rps</i> ₃	R	R	R	R	R	S	S	R	R
PRX27-108	<i>Rps</i> ₁	R	R	S	S	S	S	S	S	S
	<i>Rps</i> ₄	R	R	R	R	S	S	S	S	S
Altona	<i>Rps</i> ₆	R	R	R	R	S	S	S	S	S

^aR = resistant; S = susceptible.

Materials and methods. F₂ populations from each cross were evaluated in the greenhouse for their reaction to physiologic races 1, 2, 3, 4, 5, 7, and 9. Race 6 was not used because it is no longer available, and race 8 was not used because it would have given the same results as race 9. The F₃ generation was tested to confirm the segregation ratios obtained in the F₂ populations, but the data are not included here for brevity.

Inoculum of Pmg was prepared by growing isolates of the respective races on oatmeal agar in petri dishes for 2-3 wk at 22-24 C. Ten-day-old seedlings

were inoculated in the greenhouse by the hypocotyl method, which consisted of inserting a 2 x 2-mm piece of mycelium into a longitudinal slit in the hypocotyl and covering the wound with petrolatum to prevent desiccation of the inoculum and host tissue. The plants were incubated in the greenhouse at 24-27 C. Six days after inoculation, the seedlings were classified resistant (no visible symptoms) or susceptible (dead). Appropriate resistant and susceptible checks were included for each race with every cross. The susceptible checks averaged 98.4% dead, whereas the resistant checks ranged from 0 for Mukden to 1.6% susceptible for Altona. Chi-square test for goodness of fit to hypothesized ratios were used to analyze data from F_2 and F_3 generations.

(1) PI 273483D - Graduate student Alice Layton Hahn studied the inheritance of resistance to PI 157409 and PI 273483D for her MS thesis research. PI 157409 has been reported (Layton et al., 1984) to have the genes $Rps_1^b Rps_4^b$. The genetics of resistance in PI 273483D was not completely determined. It was found to have two genes for resistance. One of the genes is Rps_1^c and the other appears to be at the Rps_3 locus but not Rps_3 or Rps_3^b because it gives susceptibility to races 5, 7, and 9.

(2) PI 64747 - Graduate student L. Daniel Ploper studied the inheritance of resistance in PI 64747 and PI 172901. Resistance in PI 172901 was reported (Ploper et al., 1985) to be controlled by the two genes $Rps_1^b Rps_3^b$. The segregation of the F_2 populations from the crosses of PI 64747 with the eight cultivars is summarized in Table 2 and the complete data are presented in Table 7.

Table 2. The segregation of the F_2 populations from crosses of PI 64747 with cultivars containing the genes rps , Rps_1 , Rps_1^b , Rps_1^c , Rps_1^k , Rps_3 , $Rps_1 Rps_4$, Rps_6 when inoculated with races 1, 2, 3, 4, 5, 7 and 9 of *P. megasperma* f. sp. *glycinea*

PI 64747 crossed to	Gene(s)	Reaction to physiologic race ^a						
		1	2	3	4	5	7	9
Harosoy	<i>rps</i>	15:1	15:1	15:1	3:1	3:1	3:1	15:1
Mukden	Rps_1^b	R	R	15:1	3:1	3:1	3:1	15:1
Sanga	Rps_1^c	R	15:1	R	15:1	15:1	R	R
Wells II	Rps_1^k	R	R	R	3:1	3:1	R	R
Williams 82	Rps_1	R	R	R	15:1	15:1	R	R
PI 86972-1	Rps_3	R	R	R	R	R	3:1	R
PRX-27-108	$Rps_1 Rps_4$	R	R	63:1	15:1	3:1	3:1	15:1
Altona	Rps_6	63:1	63:1	63:1	15:1	3:1	3:1	15:1

^aSegregating resistant: susceptible; R = uniformly resistant.

The cross with Harosoy (*rps*) indicated that there were two genes for resistance to races 1, 2, 3, and 9; and one gene for resistance to races 4, 5, and 7. Crosses with Mukden, Sanga, Wells II, and Williams 82 indicated that one of the genes was at the *Rps*₁ locus and was probably *Rps*₁^c. The cross with PI 86972-1 (*Rps*₃) indicated that the other gene was at the *Rps*₃ locus and was probably *Rps*₃. Furthermore, the F₂ population from the cross of PI 64747 with PI 172901 (*Rps*₁^b*Rps*₃^b), Table 3, was uniformly resistant to the seven races as expected if PI 64747 has the gene *Rps*₁^c which gives resistance to races 1, 2, 3, 7, and 9, and susceptibility to races 4 and 5; and the gene *Rps*₃ which is allelic to *Rps*₃^b but gives susceptibility to race 7.

Table 3. The segregation of the F₂ populations from crosses of selected plant introductions when inoculated with races 1, 2, 3, 4, 5, 7, and 9 and *P. megasperma* f. sp. *glycinea*

Cross	Genes	Reaction to physiologic race						
		1	2	3	4	5	7	9
PI 64747 x PI 172901	<i>Rps</i> ₁ ^c <i>Rps</i> ₃ <i>Rps</i> ₁ ^b <i>Rps</i> ₃ ^b	R	R	R	R	R	R	R
PI 157404 x PI 274212	<i>Rps</i> ₁ ^b <i>Rps</i> ₄ <i>Rps</i> ₁ ^b <i>Rps</i> ₄	R	R	R	R	R	R	R
PI 64747 x PI 274212	<i>Rps</i> ₁ ^c <i>Rps</i> ₃ <i>Rps</i> ₁ ^b <i>Rps</i> ₄	R	63:1	R	63:1	15:1	R	R
PI 274212 x PI 172901	<i>Rps</i> ₁ ^b <i>Rps</i> ₄ <i>Rps</i> ₁ ^b <i>Rps</i> ₃ ^b	R	15:1	R	R	R	R	R
PI 64747 x PI 82312N	<i>Rps</i> ₁ ^c <i>Rps</i> ₃ <i>Rps</i> ₃ ^b <i>Rps</i> ₅	R	R	R	R	R	15:1	R
PI 274212 x PI 82312N	<i>Rps</i> ₁ ^b <i>Rps</i> ₄ <i>Rps</i> ₃ ^b <i>Rps</i> ₅	255:1	63:1	255:1	255:1	63:1	15:1	63:1
PI 82312N x PI 157409	<i>Rps</i> ₃ ^b <i>Rps</i> ₅ <i>Rps</i> ₁ ^b <i>Rps</i> ₄	255:1*	63:1	255:1*	255:1	63:1	15:1	63:1

*Were uniformly resistant probably because of small number of plants.

(3) PI 274212 - The segregation ratios of the F_2 populations from crosses of PI 274212 with each of the eight cultivars when inoculated with races 1, 2, 3, 4, 5, 7, and 9 of Pmg are presented in Table 4 and the complete data in Table 8.

Table 4. The segregation of the F_2 populations from crosses of PI 274212 with cultivars containing the genes rps , Rps_1 , Rps_1^b , Rps_1^c , Rps_1^k , Rps_3 , Rps_1 , Rps_4 , Rps_6 when inoculated with races 1, 2, 3, 4, 5, 7, and 9 of *P. megasperma* f. sp. *glycinea*

PI 274212 crossed to	Gene(s)	Reaction to physiologic race						
		1	2	3	4	5	7	9
Harosoy	rps	15:1	3:1	15:1	15:1	3:1	3:1	3:1
Mukden	Rps_1	R	15:1	15:1	15:1	3:1	3:1	--
Sanga	Rps_1^b	R	3:1	R	R	R	R	R
Wells II	Rps_1^c	R	15:1	R	15:1	3:1	R	R
Williams 82	Rps_1^k	R	15:1	R	R	R	R	R
PI 85972-1	Rps_3	63:1	15:1	63:1	63:1	15:1	3:1	15:1
PRX27-108	Rps_1 Rps_4	R	R	R	R	3:1	3:1	3:1
Altona	Rps_6	63:1	15:1	63:1	63:1	3:1	3:1	3:1

The cross with Harosoy indicated two genes for resistance in PI 274212 to races 1, 3, and 4; and one gene for resistance to races 2, 5, 7, and 9. The crosses with Mukden, Sanga, Wells II, and Williams 82 indicated that one of the genes was at the Rps_1 locus but was not effective against race 2 and was probably Rps_1^b . The other gene gave resistance to races 1, 2, 3, and 4, and susceptibility to races 5, 7, and 9. The cross with PRX27-108 suggested that this gene was at the Rps_4 locus and gave the same reactions as Rps_4 to the races used. The genotype of PI 274212 appears to be $Rps_1^b Rps_4$, the same as reported for PI 157409. The F_2 population from the cross of PI 274212 x PI 157409 was uniformly resistant when inoculated with the seven races (Table 3), indicating that they have the same genotype. Also, the F_2 populations of PI 274212 crossed with PI 64747 ($Rps_1^b Rps_3^b$), Table 3, segregated in the ratios expected if PI 274212 had the two genes Rps_1^b , which gives resistance to races 1, 3, 4, 5, 7, and 9; and Rps_4 , which gives resistance to races 1, 2, 3, and 4.

(4) PI 82312N - The segregation of the F_2 populations from the crosses of PI 82312N with the eight cultivars is summarized in Table 5 and the complete

data are presented in Table 9. The cross with Harosoy (*rps*) indicated two genes for resistance to races 1, 2, 3, 4, 5, and 9; and one gene for resistance to race 7. The crosses with Mukden, Sanga, Wells II, and Williams 82 indicated that neither gene was at the *Rps*₁ locus. The F₂ population from the cross with PI 86972-1 (*Rps*₃) was resistant to races 1, 2, 3, 4, 5, and 9, which suggested that *Rps*₃ from PI 86972-1 was allelic to one of the genes in PI 82312N. The segregation in the F₂ populations from all crosses inoculated with races 5, 7, and 9 indicated that one of the genes gave resistance to races 1, 2, 3, 4, 5, 7, and 9, whereas the other gene gave resistance to races 1, 2, 3, 4, 5, and 9. Since one of the genes is at the *Rps*₃ locus, it could be either *Rps*₃ or *Rps*₃^b. If it is *Rps*₃^b, the other gene would condition resistance to races 1, 2, 3, 4, 5, and 9, and susceptibility to race 7. *Rps*₅ would satisfy this requirement. However, if the gene at the *Rps*₃ locus is *Rps*₃, then the other gene must give resistance to race 7 and could not be *Rps*₅. The data do not discriminate these two possibilities. However, the F₂ population from the cross of PI 172901 (*Rps*₁^b*Rps*₃^b) with PI 82312N (Table 3) was uniformly resistant to race 7, indicating that the gene at the *Rps*₃ locus in PI 82312N is *Rps*₃^b. The other gene is probably *Rps*₅. Crosses of PI 82312N with PI 64747 (*Rps*₁^c*Rps*₃) and PI 157409 (*Rps*₁^b*Rps*₄), Table 3, give additional evidence. F₃ lines resistant to races 1, 2, 3, 4, 5, and 9, and either resistant or susceptible to race 7 were selected from the cross of PI 82312N with Harosoy to determine if they actually contain *Rps*₃^b and *Rps*₅, respectively.

Table 5. The segregation of the F₂ population from crosses of PI 82312N with cultivars containing the genes *rps*, *Rps*₁, *Rps*₁^b, *Rps*₁^c, *Rps*₁^k, *Rps*₃, *Rps*₁*Rps*₄, and *Rps*₆ when inoculated with races 1, 2, 3, 4, 5, 7, and 9 of *P. megasperma* f. sp. *glycinea*

PI 82312N crossed to	Gene(s)	Reaction to physiologic race						
		1	2	3	4	5	7	9
Harosoy	<i>rps</i>	15:1	15:1	15:1	15:1	15:1	3:1	15:1
Mukden	<i>Rps</i> ₁	63:1	63:1	15:1	15:1	15:1	3:1	15:1
Sanga	<i>Rps</i> ₁ ^b	63:1	15:1	63:1	63:1	63:1	15:1	63:1
Wells II	<i>Rps</i> ₁ ^c	63:1	63:1	63:1	15:1	15:1	15:1	63:1
Williams 82	<i>Rps</i> ₁ ^k	63:1	63:1	63:1	63:1	63:1	15:1	63:1
PI 86972-1	<i>Rps</i> ₃	R	R	R	R	R	3:1	R
PRX27-108	<i>Rps</i> ₁ <i>Rps</i> ₄	255:1	255:1	63:1	63:1	15:1	3:1	15:1
Altona	<i>Rps</i> ₆	63:1	63:1	63:1	63:1	15:1	3:1	15:1

(5) PI 340046 - The segregation ratios from the F_2 populations from the crosses of PI 340046 with the eight cultivars are summarized in Table 6 and the complete data are presented in Table 10. F_2 population from the cross with Harosoy (*rps*) indicates that there are two genes for resistance in PI 340046 to races 1, 2, 3, and 4, but only one gene for resistance to races 5, 7, and 9. Crosses with Mukden, Sanga, Wells II, and Williams 82 indicated that one of the genes was at the Rps_1 locus and was probably Rps_1^k . The cross with PI 86972-1 indicated that the other gene is at the Rps_3 locus but is not Rps_3 because it is not effective against races 5 and 9. The new symbol rps_3^c is proposed for this gene which gives resistance to races 1, 2, 3, and 4, and susceptibility to races 5, 7, and 9. Rps_3^c can be distinguished from Rps_1^b , Rps_1^c , Rps_1^k , Rps_3 , and Rps_5 because it gives resistance to race 12, and from Rps_6 by its resistance to race 13. It cannot readily be distinguished from Rps_4 except by studying the progeny from crosses between cultivars containing Rps_3^c and Rps_4 .

Table 6. The segregation of the F_2 populations from crosses of PI 340046 with cultivars containing the genes *rps*, Rps_1 , Rps_1^b , Rps_1^c , Rps_1^k , Rps_3 , Rps_1 , Rps_4 , and Rps_6 when inoculated with races 1, 2, 3, 4, 5, 7, and 9 of *P. megasperma* f. sp. *glycinea*

PI 340046 crossed to	Gene(s)	Reaction to physiologic race						
		1	2	3	4	5	7	9
Harosoy	<i>rps</i>	15:1	15:1	15:1	15:1	3:1	3:1	3:1
Mukden	Rps_1	R	R	15:1	15:1	3:1	3:1	3:1
Sanga	Rps_1^b	R	15:1	R	R	R	R	R
Wells II	Rps_1^c	R	R	R	15:1	3:1	R	R
Williams 82	Rps_1^k	R	R	R	R	R	R	R
PI 86972-1	Rps_3	R	R	R	R	15:1	3:1	3:1
PRX27-108	Rps_1 Rps_4	R	R	63:1	63:1	3:1	3:1	3:1
Altona	Rps_6	63:1	63:1	63:1	63:1	3:1	3:1	3:1

Table 7. Segregation of F_2 populations from crosses of PI 64747 with Harosoy, Mukden, Sanga, Wells II, Williams 82, PI 86972-1, and PRX27-108 to seven physiologic races of *P. megasperma* f. sp. *glycinea*

Parentage & gene	Race	Number of Plants ^a			Ratio ^b	χ^2	P
		Total	Res	Susc			
PI 64747 X	1	212	201	11	15:1	0.4075	0.70-0.50
	2	236	222	14	15:1	0.0406	0.90-0.80
Harosoy (<i>rps</i>)	3	248	232	16	15:1	0.0172	0.90-0.80
	4	239	174	65	3:1	0.6150	0.50-0.30
	5	262	188	74	3:1	1.4707	0.30-0.20
	7	208	155	53	3:1	0.0256	0.90-0.80
	9	205	194	11	15:1	0.2734	0.70-0.50
Mukden (<i>Rps</i> ₁) X	1	204	204	0	R		
	2	205	205	0	R		
PI 64747	3	231	221	10	15:1	1.4548	0.30-0.20
	4	225	173	52	3:1	0.4281	0.70-0.50
	5	228	177	51	3:1	0.8421	0.50-0.30
	7	170	137	33	3:1	2.8313	0.10-0.05
	9	167	155	12	15:1	0.2495	0.70-0.50
PI 64747 X	1	246	246	0	R		
	2	248	227	21	15:1	2.0817	0.20-0.10
Sanga (<i>Rps</i> ₁ ^b)	3	257	257	0	R		
	4	262	252	10	15:1	2.6473	0.20-0.10
	5	247	228	19	15:1	0.8769	0.50-0.30
	7	206	206	0	R		
	9	188	188	0	R		
PI 64747 X	1	221	221	0	R		
	2	228	228	0	R		
Wells II (<i>Rps</i> ₁ ^c)	3	245	245	0	R		
	4	251	185	66	3:1	0.2244	0.70-0.50
	5	261	188	73	3:1	1.2273	0.30-0.20
	7	205	205	0	R		
	9	196	196	0	R		
Williams 82 (<i>Rps</i> ₁ ^k) X	1	210	210	0	R		
	2	212	212	0	R		
PI 64747	3	195	195	0	R		
	4	207	193	14	15:1	0.0930	0.90-0.80
	5	199	187	12	15:1	0.0164	0.90-0.80
	7	221	221	0	R		
	9	235	235	0	R		
PI 64747 X	1	189	189	0	R		
	2	211	211	0	R		
PI 86972-1 (<i>Rps</i>)	3	254	254	0	R		
	4	210	210	0	R		
	5	235	235	0	R		
	7	172	140	32	3:1	3.7519	0.10-0.05
	9	186	186	0	R		

Table 7. *Continued*

Parentage & gene	Race	Number of Plants ^a			Ratio ^b	χ^2	P
		Total	Res	Susc			
PI 64747 X	1	249	249	0	R		
	2	236	236	0	R		
PRX27-108 (<i>Rps₁Rps₄</i>)	3	217	215	2	63:1	0.5794	0.50-0.30
	4	181	169	12	15:1	0.0445	0.90-0.80
	5	243	185	58	3:1	0.1659	0.70-0.50
	7	190	139	51	3:1	0.3438	0.70-0.50
	9	187	178	9	15:1	0.6591	0.50-0.30
PI 64747 X	1	163	162	1	63:1	0.9544	0.50-0.30
	2	158	157	1	63:1	0.8876	0.50-0.30
Altona (<i>Rps₆</i>)	3	169	167	2	63:1	0.1578	0.70-0.50
	4	167	153	14	15:1	1.2970	0.30-0.20
	5	174	120	54	3:1	3.3793	0.10-0.05
	7	162	113	49	3:1	2.3786	0.20-0.10
	9	171	159	12	15:1	0.1719	0.70-0.50

^aAbbreviations: Res = resistant, Susc = susceptible.

^bRatio: Resistant:susceptible, R = resistant.

Table 8. Segregation of F_2 populations from crosses of PI 274212 with Harosoy, Mukden, Sanga, Wells II, Williams 82, PI 86972-1, and PRX27-108 to seven physiologic races of *P. megasperma* f. sp. *glycinea*

Parentage & gene	Race	Number of Plants ^a			Ratio ^b	χ^2	P
		Total	Res	Susc			
PI 274212 X	1	253	231	22	15:1	2.5826	0.20-0.10
	2	273	212	61	3:1	1.0268	0.30-0.20
Harosoy (<i>rps</i>)	3	207	195	12	15:1	0.0724	0.80-0.70
	4	266	246	20	15:1	0.7308	0.50-0.30
	5	263	194	69	3:1	0.2141	0.70-0.50
	7	261	194	67	3:1	0.0625	0.90-0.80
	9	242	190	52	3:1	1.5922	0.30-0.20
Mukden (<i>Rps₁</i>) X	1	235	235	0	R		
	2	197	182	15	15:1	0.6257	0.50-0.30
PI 274212	3	132	121	11	15:1	0.9777	0.50-0.30
	4	149	144	5	15:1	2.1302	0.20-0.10
	5	87	59	29	3:1	3.0038	0.10-0.05
	7	230	175	55	3:1	0.1449	0.80-0.70
	9	--	--	--			

Table 8. *Continued*

Parentage and gene	Race	Number of plants ^a			Ratio ^b	χ^2	P
		Total	Res	Susc			
PI 274212 X	1	168	168	0	R		
Sanga (<i>Rps</i> ₁ ^b)	2	156	127	29	3:1	3.4188	0.10-0.05
	3	125	125	0	R		
	4	156	156	0	R		
	5	183	183	0	R		
	7	186	186	0	R		
	9	161	161	0	R		
PI 274121 X	1	254	254	0	R		
Wells II (<i>Rps</i> ₁ ^c)	2	249	229	20	15:1	1.3496	0.30-0.20
	3	215	215	0	R		
	4	270	254	16	15:1	0.0483	0.90-0.80
	5	238	169	69	3:1	2.0224	0.20-0.10
	7	250	250	0	R		
	9	210	210	0	R		
PI 274212 X	1	257	257	0	R		
Williams 82 (<i>Rps</i> ₁ ^k)	2	261	241	20	15:1	0.8891	0.50-0.30
	3	119	119	0	R		
	4	253	253	0	R		
	5	186	186	0	R		
	7	213	213	0	R		
	9	184	184	0	R		
PI 274212 X	1	273	271	2	63:1	1.2224	0.30-0.20
PI 86972-1 (<i>Rps</i> ₃)	2	273	249	24	15:1	3.0087	0.10-0.05
	3	166	165	1	63:1	0.9948	0.50-0.30
	4	215	211	4	63:1	0.1241	0.80-0.70
	5	193	176	17	15:1	2.1557	0.20-0.10
	7	230	180	50	3:1	1.3043	0.30-0.20
	9	187	170	17	15:1	2.5757	0.20-0.10
PI 274212 X	1	244	244	0	R		
PRX27-108 (<i>Rps</i> ₁ <i>Rps</i> ₄)	2	255	255	0	R		
	3	149	148	1	R		
	4	227	227	0	R		
	5	186	132	54	3:1	1.6129	0.30-0.20
	7	274	199	75	3:1	0.8223	0.50-0.30
	9	180	131	49	3:1	0.4740	0.50-0.30
PI 274212 X	1	159	157	2	63:1	0.0959	0.80-0.70
Altona (<i>Rps</i> ₆)	2	149	137	12	15:1	0.8273	0.50-0.30
	3	126	125	1	63:1	0.5000	0.50-0.30
	4	141	137	4	63:1	1.4911	0.30-0.20
	5	162	132	30	3:1	3.6147	0.10-0.05
	7	167	136	31	3:1	3.6906	0.10-0.05
	9	154	125	29	3:1	3.1255	0.10-0.05

^aAbbreviations: Res = resistant, Susc = susceptible.^bRatio = resistant:susceptible, R = resistant.

Table 9. Segregation of F_2 populations from crosses of PI 82312N with Harosoy, Mukden, Sanga, Wells II, Williams 82, PI 86972-1, PRX27-108, and Altona to seven physiologic races of *P. megasperma* f. sp. *glycinea*

Parentage and gene	Race	Number of plants ^a			Ratio ^b	χ^2	P
		Total	Res	Susc			
PI 82312N	1	266	254	12	15:1	1.3724	0.30-0.20
	2	269	251	18	15:1	0.0894	0.80-0.70
X Harosoy (<i>rps</i>)	3	191	173	18	15:1	3.2841	0.10-0.05
	4	265	244	21	15:1	1.2681	0.30-0.20
	5	178	169	9	15:1	0.4329	0.70-0.50
	7	267	203	64	3:1	0.1510	0.70-0.50
	9	257	234	23	15:1	3.1961	0.10-0.05
PI 82312N	1	272	266	6	63:1	0.7320	0.50-0.30
	2	276	272	4	63:1	0.0230	0.90-0.80
X Mukden (<i>Rps</i> ₁)	3	211	193	18	15:1	1.8733	0.20-0.10
	4	234	221	13	15:1	0.1925	0.70-0.50
	5	204	190	14	15:1	0.1307	0.80-0.70
	7	235	165	70	3:1	2.8723	0.10-0.05
	9	255	240	15	15:1	0.0588	0.90-0.80
PI 82312N	1	265	256	8	63:1	3.6839	0.10-0.05
	2	252	230	22	15:1	2.6455	0.20-0.10
X Sanga (<i>Rps</i> ₁ ^b)	3	91	86	3	63:1	1.8505	0.20-0.10
	4	246	244	2	63:1	0.8984	0.50-0.30
	5	238	233	5	63:1	0.4484	0.70-0.50
	7	215	201	14	15:1	0.0251	0.90-0.80
	9	235	232	3	63:1	0.1248	0.80-0.70
PI 82312N	1	238	236	2	63:1	0.8069	0.50-0.30
	2	246	242	4	63:1	0.0064	0.95-0.90
X Wells II (<i>Rps</i> ₁ ^c)	3	148	147	1	63:1	0.7567	0.50-0.30
	4	248	232	16	15:1	0.0172	0.90-0.80
	5	231	216	15	15:1	0.0233	0.90-0.80
	7	252	236	16	15:1	0.0042	0.95-0.90
	9	203	201	2	63:1	0.4398	0.70-0.50
Williams 82 (<i>Rps</i> ₁ ^k)	1	255	250	5	63:1	0.2629	0.70-0.50
	2	243	236	7	63:1	2.7451	0.10-0.05
X PI 82312N	3	217	215	2	63:1	0.5794	0.50-0.30
	4	253	251	2	63:1	0.9802	0.50-0.30
	5	237	231	6	63:1	1.4472	0.30-0.20
	7	239	225	14	15:1	0.0627	0.90-0.80
	9	211	206	5	63:1	0.8937	0.50-0.30
PI 82312N	1	268	268	0	R		
	2	263	263	0	R		
X PI 86972-1 (<i>Rps</i> ₃)	3	270	266	0	R		
	4	270	270	0	R		
	5	256	256	0	R		
	7	242	185	57	3:1	0.2699	0.70-0.50
	9	266	266	0	R		

Table 9. *Continued*

Parentage and gene	Race	Number of plants ^a			Ratio ^b	χ^2	P
		Total	Res	Susc			
PI 82312N X	1	262	260	2	255:1	0.9354	0.50-0.30
	2	245	244	1	255:1	0.0019	0.98-0.95
PRX27-108 (<i>Rps</i> ₁ <i>Rps</i> ₄)	3	214	209	5	63:1	0.8334	0.50-0.30
	4	269	266	3	63:1	0.3498	0.70-0.50
	5	201	183	18	15:1	2.5104	0.20-0.10
	7	264	188	76	3:1	2.0202	0.20-0.10
	9	251	239	12	15:1	0.9245	0.50-0.30
PI 82312N	1	151	148	3	63:1	0.1767	0.70-0.50
	2	138	136	2	63:1	0.0115	0.95-0.90
X Altona (<i>Rps</i> ₆)	3	128	127	1	63:1	0.5079	0.50-0.30
	4	128	127	1	63:1	0.5079	0.50-0.30
	5	155	150	5	15:1	2.4193	0.20-0.10
	7	125	100	25	3:1	1.6666	0.20-0.10
	9	135	126	9	15:1	0.0400	0.90-0.80

^aAbbreviations: Res = resistant, Susc = susceptible.

^bRatio = resistant to susceptible, R = resistant.

Table 10. Segregation of the F₂ populations from crosses of PI 340046 with Harosoy, Mukden, Sanga, Wells II, Williams 82, PI 86972-1, PRX27-108, and Altona to seven physiologic races of *P. megasperma* f. sp. *glycinea*

Parentage and gene	Race	Number of plants ^a			Ratio ^b	χ^2	P
		Total	Res	Susc			
PI 340046 X	1	257	242	15	15:1	0.0749	0.80-0.70
	2	248	239	9	15:1	2.9075	0.10-0.05
Harosoy (<i>rps</i>)	3	229	219	10	15:1	1.3860	0.30-0.20
	4	256	245	11	15:1	1.6666	0.30-0.10
	5	179	156	23	3:1	14.0949	>0.01
	7	266	208	58	3:1	1.4486	0.30-0.20
	9	215	168	47	3:1	1.1302	0.30-0.20
Mukden (<i>Rps</i> ₁) X	1	268	268	0	R		
	2	269	269	0	R		
PI 340046	3	219	206	13	15:1	0.0368	0.90-0.80
	4	264	248	16	15:1	0.0161	0.90-0.80
	5	161	129	32	3:1	2.2546	0.20-0.10
	7	271	210	61	3:1	0.8966	0.50-0.30
	9	256	198	58	3:1	0.7500	0.50-0.30

Table 10. *Continued*

Parentage and gene	Race	Number of plants ^a			Ratio ^b	χ^2	P
		Total	Res	Susc			
PI 340046 X Sanga (<i>Rps</i> ₁ ^b)	1	263	263	0	R	2.7428	0.10-0.05
	2	224	216	8	15:1		
	3	63	63	0	R		
	4	232	232	0	R		
	5	89	89	0	R		
	7	222	222	0	R		
	9	89	89	0	R		
PI 340046 X Wells II (<i>Rps</i> ₁ ^c)	1	203	203	0	R	0.1251 15.1172	0.80-0.70 >0.01
	2	138	138	0	R		
	3	267	267	0	R		
	4	235	219	16	15:1		
	5	199	173	26	3:1		
	7	239	239	0	R		
	9	236	236	0	R		
Williams 82 (<i>Rps</i> ₁ ^k) X PI 340046	1	261	261	0	R		
	2	258	258	0	R		
	3	200	200	0	R		
	4	273	273	0	R		
	5	207	207	0	R		
	7	249	249	0	R		
	9	244	244	0	R		
PI 340046 X PI 86972-1 (<i>Rps</i> ₃)	1	259	259	0	R	0.1523 0.1424 1.1520	0.70-0.50 0.80-0.70 0.30-0.20
	2	276	276	0	R		
	3	74	73	1	R		
	4	218	218	0	R		
	5	112	106	6	15:1		
	7	234	178	56	3:1		
	9	107	103	4	15:1		
PI 340046 X PRX27-108 (<i>Rps</i> ₁ <i>Rps</i> ₄)	1	246	269	0	R	0.4931 0.2198 9.8136 0.8600 1.7142	0.50-0.30 0.70-0.50 >0.01 0.50-0.30 0.20-0.10
	2	273	273	0	R		
	3	208	206	2	63:1		
	4	260	255	5	63:1		
	5	186	158	28	3:1		
	7	262	203	59	3:1		
	9	252	198	54	3:1		
PI 340046 X Altona (<i>Rps</i> ₆)	1	237	234	3	63:1	0.1356 1.4996 1.3122 0.5794 1.4267 0.3218 1.8469	0.80-0.20 0.30-0.20 0.30-0.20 0.50-0.30 0.30-0.20 0.70-0.50 0.20-0.10
	2	235	229	6	63:1		
	3	189	188	1	63:1		
	4	217	215	2	3:1		
	5	219	172	47	3:1		
	7	233	171	62	3:1		
	9	122	98	24	3:1		

^aAbbreviations: Res = resistant, Susc = susceptible.^bRatio = resistant:susceptible, R = resistant.

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1) Screening for cytoplasmic/maternal effects in resistance to soybean cyst nematode.

With the discovery of soybean cyst nematode (SCN) in the U.S. in 1954, the research for resistance was initiated. Ross and Brim (1957) identified several soybean plant introductions resistant to the North Carolina SCN populations. Epps and Hartwig (1972) reported PI lines resistant to race 4. Extensive screening of germplasm by Anand and Gallo (1984) and Anand, Wrather and Shumway (1985) resulted in the isolation of several additional sources of resistance to races of SCN. Caldwell, Brim and Ross (1960) and Thomas et al. (1975) studied inheritance of SCN resistance in several crosses of soybean. Presumably, all of these reported sources of resistance pertain to nucleargenic only. Therefore, we attempted to observe any of the existing cytoplasmic/maternal effects for SCN resistance. Such effects, if any, would be utilized in breeding programs to broaden the genetic/cytoplasmic base for SCN resistance.

An experiment was conducted in the greenhouse during fall of 1985. The parents, 'Essex', 'Peking', PI 90763, PI 88788 and PI 437654 were crossed in the field during summer 1985 to generate F_1 s and their reciprocals. Ten F_1 plants of each cross, including reciprocals, were tested for their reaction to different races of SCN. Each plant was inoculated with one thousand eggs and larvae.

The details of the greenhouse screening tests were essentially those described by Anand et al. (1985). The results are presented in Table 1.

In all cases except one, there was no significant difference between the F_1 s in their reciprocal crosses for the number of cysts per plant. This indicated that there was no cytoplasmic/maternal effects for SCN resistance. In all cases except one, the F_1 reaction for the cyst number was less than the susceptible parent indicating incomplete dominance for susceptibility. Since Peking and PI 88788 are resistant to race 3, the nature of resistance in the F_1 s appears to show that the genes for resistance to this race are allelic.

Table 1. Number of white females (cysts) per plant against races 3, 4, and 5 of soybean cyst nematode

Cross no.	Soybean cross or line	SCN race		
		3	4	5
1	Essex x PI 88788	89	138	218
2	PI 88788 x Essex	92	122	142
3	Peking x PI 88788	2	93	117
4	PI 88788 x Peking	1	67	112
5	PI 88788 x PI 90763	--	32	119
6	PI 90763 x PI 88788	--	26	110
7	Essex x PI 437654	--	--	192
8	PI 437654 x Essex	--	--	210
9	Essex (check)	150	180	216
10	Peking (check)	0	52	8
12	PI 90763 (check)	1	89	1
13	PI 88788 (check)	6	7	159
14	PI 437654 (check)	0	0	0
	LSD (5%)	31	32	38

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1) Genetics of reaction to soybean mosaic virus (SMV) in the cultivars
'Kwanggyo', 'Marshall', and PI 96983.

Several genes conditioning resistance to SMV have been found and some have been assigned gene symbols. In addition, a series of SMV strain groups has been differentiated by their interactions with a selected group of cultivars (Cho and Goodman, 1979; Lim, 1985). We have undertaken a study of the genes conditioning the reactions of certain differential cultivars to SMV in an attempt to establish their relationships with symbolized genes. Recently, we have established the number of genes conditioning SMV resistance in each of the cultivars Kwanggyo, Marshall and PI 96983.

The isolate SMV-VA, which was classified into Cho and Goodman's strain group G1 (Hunst and Tolin, 1982), was used to inoculate F_3 lines from crosses shown in Table 1. All work was done under field conditions using methods described by Roane et al. (1983). We found that PI 96983 has two genes conditioning reaction to SMV-VA and that Kwanggyo and Marshall each have one gene; these are either allelic or are very closely linked.

Table 1. Segregation of F_3 lines for reaction to SMV-VA (= G1)

Cross	Classes and frequencies			χ^2	Ratio tested	P
	Homozygous resistant	Segregating	Homozygous susceptible			
PI 96983 x Essex (RXS)	69	71	9	0.465	7:8:1	>0.7
Essex x Marshall (SXR)	47	80	51	1.421	1:2:1	>0.3
Kwanggyo x Lee 68 (RXS)	30	48	15	4.935	1:2:1	>0.05
Kwanggyo x Marshall (RXR)	82	2 ⁺	0	-	-	-

⁺Two lines segregated 16:1 and 23:2.

Kiihl and Hartwig (1979) identified one gene, *RSV*, in PI 96983. They used isolates of SMV which were later assigned by Cho and Goodman (1982) to strain groups G2 and G3. These strains must have one or more virulence genes capable of defeating one of the resistance genes in PI 96983. Similarly, Buzzell and Tu (1984) detected only one gene in a PI 96983 descendant, L78-379. Either the strains they used, G7 and G7A, can also defeat one of the genes in PI 96983, or else only one of the two genes from PI 96983 occurs in L78-379.

The single genes found to condition the resistance of Kwanggyo and Marshall to SMV have not yet been tested against any other symbolized gene, but we plan to conduct such experiments. At present, we are concerned about the poor fit of the Kwanggyo x Lee 68 cross to a monogenic ratio. When we produced the F_3 seed in the field, the F_2 plants were inoculated with SMV and some failed to produce seed. This may have brought about a deficiency of homozygous susceptible lines. Kwanggyo will be given further attention.

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2) Application of the gene-for-gene hypothesis to soybean-soybean mosaic virus interactions

The gene-for-gene hypothesis has been found applicable to several host-parasite interactions in which the parasite is a fungus. It has most satisfactorily explained interactions involving cereal rust and powdery mildew diseases in which cases the pathogens are obligate parasites and the genes of both the parasites and hosts may be manipulated in genetic tests. Generally, the gene-for-gene hypothesis has not been applied to host-virus systems because virulence genes in viruses cannot be manipulated by hybridization. However, by assuming that each having soybean mosaic virus (SMV) strain possesses one or no virulence gene (having no virulence gene means that the strain can cause symptoms only in a host having no resistance gene), we may soon be able to "read out" host genotypes for resistance to SMV simply by inoculating cultivars with carefully selected SMV strains. Such a system has been described for *Phaseolus vulgaris* and bean common mosaic virus (Drijfhout, 1978).

In Table 1, the cumulative genetic research on SMV resistance in soybean is summarized. Information is taken from published works of Buzzell and Tu (1984); Cho and Goodman (1979, 1982); Kiihl and Hartwig (1979); Lim (1985); and Roane, Tolin and Buss (1983, 1986). From Table 1, it may be seen that:

1. PI 96983, carrying *Rsv*, segregates monogenically when progenies of its crosses are inoculated with SMV strains G2, G3, G6, G7, G7A, and C14 (Buzzell and Tu, 1984; Kiihl and Hartwig, 1979; Lim, 1985), but digenically when inoculated with G1 (Roane et al., 1986). Therefore, PI 96983 must have a second resistance gene labelled here *Rsv*?
2. Strains G2, G3, G6, G7, G7A, and C14 each must possess a virulence gene capable of "defeating" one of the genes in PI 96983 but G1 must lack such a virulence gene. This is also apparent from Table 1 where it is shown that G1 does not produce symptoms on cultivars carrying resistance genes; therefore, G1 should be used in all genetic studies because it should detect any resistance gene.
3. If strains G2, G3, G6, G7, G7A, and C14 each possess a single virulence gene, progenies of some cultivars other than PI 96983, which showed monogenic inheritance when inoculated with one of these strains, could show digenic inheritance when progenies are inoculated with G1. Note that our assumptions do not preclude the possibility that some virus strains may have more than one virulence gene.

4. 'Ogden' has been assumed to have a gene, rsv^t , at the *Rsv* locus (Kiihl and Hartwig, 1979). However, this gene may be allelic with *Rsv*?, the second gene in PI 96983, rather than with *Rsv*. Proof of this hypothesis requires the inoculation of partitioned F_3 lines of PI 96983 x Ogden and a susceptible cv. x Ogden with strains G1 and G2 or G3.
5. 'York' has been assumed to carry rsv^t because of its descent from 'Tokyo', Ogden, and 'Hood' (Kiihl and Hartwig, 1979; Roane et al., 1983). York is a selection from a cross of 'Dorman' x Hood. Cho and Goodman (1982) have placed York in the cultivar group with 'Davis', Dorman and 'Ware'. Thus, York could have derived a gene for SMV resistance from either Hood or Dorman. A genetic study of York x PI 96983, York x Ogden and York x Davis using G1 and G2 to inoculate partitioned F_3 lines from the crosses will be necessary to determine if York carries rsv^t or *Rsv*?, the second gene in PI 96983.
6. By virtue of their identical responses to virus strains, 'Raiden' and 'Suweon 97' belong to the same cultivar group; therefore, Suweon 97 must carry *Rsv*₂ (Buzzell and Tu, 1984; Cho and Goodman, 1982). Since this is assumed but not proven, the Suweon 97 gene is labelled *Rsv*₂?
7. 'Kwanggyo' and 'Marshall' have alleles or closely linked genes as shown in the previous report (Roane et al., 1986). Their responses to seven SMV strains differ; therefore, they must not have the same gene or allele.
8. Lim (1985) reported a gene in PI 486355 which segregated independently of *Rsv* and *Rsv*₂ (*Rsv*₃? in Table 1) but which was not labelled. Crosses of PI 486355 with Ogden, Marshall, Kwanggyo and York are needed to find out if the PI 486355 gene is unique.

Obviously, the several assumptions for the eight points above require proof. To be able to designate properly the genes involved in SMV reactions requires that the strains of SMV and the differential cultivars be maintained by someone or at some laboratory. At present, we have samples of Cho and Goodman's strain groups G1-G7 in storage and have seed of their differential cultivars. However, we do not have Raiden, Suweon 97 or PI 486355. In addition, we urge that researchers obtaining results relative to this problem should communicate their results promptly to other interested persons so that effort will not be duplicated.

Table 1. Summary of soybean mosaic virus strains, cultivars for differentiating them, and genetics of their interactions

Virus strain group and systemic symptoms for strain/host interaction											
Cultivars ^a	Genes in cultivars	(SMV-VA) ^b									
		(SMV-1)					(SMV-1B)				
		G1	G2	G3	G4	G5	G6	G7	G7A	CL4	
		0	1	1	?	?	1	1	1	1	1
Genes in strains											
PI 96983 (Buffalo)	Rsv + Rsv [?]	0 ^c (2) ^d R6 ^e	0(1) K,L	0(1) K	0	0	0(1) B	N(1) B,L	0(1) B	0(1) L	
Ogden (Tokyo, Hood)	rsv ^t	0	0(1) K	N(1) K	0	0	0	N	-	-	
Davis (Dorman, York, Ware)	Rsv [?] ^f	0(1) R3	0	0	N	S	S	S	-	-	
Raiden = PI 360844 (Suweon 97)	Rsv ₂	0	0	0	0	0	0(1) B	0	0(1) B	N(1) L	
Suweon 97 = PI 483084 (Raiden)	Rsv ₂ [?]	0	0(1) L	0	0	0	0	0(1) L	-	N(1) L	
PI 483355	Rsv ₃	0	0	0	0	0	0	0(1) L	S	0(1) L	
Marshall	Rsv [?]	0(1) R6	N	N	0	0	N	N	-	-	
Kwanggyo	Rsv [?]	0(1) R6	0	0	0	N	N	N	-	-	

^aCultivars in parentheses give same reactions to strains as those accompanying them but not in parentheses.

^bViruses in parentheses are synonyms for the G strains.

^cSymptoms reported: 0 = no symptoms, N = systemic necrosis, S = systemic mottling, - = no report.

^dNumber of genes in a host conditioning the reaction to a strain group.

^eLetters on second line in each cluster refer to published reports -- B = Buzzell & Tu, 1984; K = Kihl & Hartwig, 1979; L = Lim, 1985; R3 = Roane, Tolin & Buss, 1983; R6 = Roane, Tolin & Buss, 1986.

^fRsv? connotes dominant resistance, the four Rsv?'s shown may or may not be alleles.

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1) A new mutation at the *ms1* locus.

Five different populations have been recognized as sources of *ms1* alleles. Genetic studies of male-sterile, female-fertile mutations conducted by Palmer et al. (1978) showed that *ms1*-North Carolina (T260), *ms1*-Urbana (T266), *ms1*-Tonica (T267), and *ms1*-Ames (T268) are independent mutations at the *ms1* locus. Yee and Jian (1983) reported another mutation at the *ms1* locus, designated Shennong Male-Sterile Soybean L-78-387.

The objective of our study is to determine if a spontaneous mutation that occurred within progeny developed from AP6(S1)C1 population is associated with the *ms1* locus.

Materials and methods: One hundred S_1 seeds of AP6(S1)C1 were planted in the spring of 1979 in Ron Secrist's plant nursery, and 55 single plants were harvested that fall. Among $S_{4:5}$ hill plots, one hill plot segregated for sterility. Figure 1 shows the origin of this hill. Twelve $S_{5:6}$ progenies (8 of fertile, 4 of sterile plants) were grown in Ames in 1985. Classification for male sterility and fertility involved the stainability of pollen grains in I_2KI and pod set at maturity. Testcrossing was conducted by using homozygous recessive *ms1*-Urbana plants as female parents and heterozygotes of the new mutants as male parents. Sixty-nine F_1 seeds were obtained for the allelism test. Thirty-one F_1 seeds were grown during fall/winter 1985 at the UPR/ISU Soybean Breeding Nursery in Isabela, Puerto Rico. They were classified for male-sterility/fertility on the basis of pollen staining.

Results: The new mutations arose in a population characterized by very complicated nuclear genetic background. AP6(S1)C1 population was derived by intermating and recurrent selection procedure from 40 strains of Group 0 to Group IV maturity (Fehr and Ortiz, 1975). It is worth mentioning that in this same population a partially male-sterile mutant *m_{sp} m_{sp}* was found in 1974/75. Expression of *m_{sp} m_{sp}* genes influenced different flower size and morphology, anther and pollen appearance, and phenotype at maturity (Stelly and Palmer, 1980).

Unknown sterile mutants showed similarities to the pattern of abnormalities caused by the *ms1* alleles. They exhibited prolonged vegetative growth

and produced large coenocytic pollen grains. Sterile plants had approximately 5.1 pods, with 5.9 seeds. Sterile *msl*-Urbana plants had 7.1 pods, with 14.9 seeds.

Among eight single-plant progenies observed in 1985, six progenies segregated for sterility, two did not. Within segregating progenies, 392 plants were fertile, 140 plants were sterile; that fit a ratio of 3:1, chi-square = 0.4912, $P = 0.10-0.50$ (Table 1).

$S_{5:6}$ progenies of four sterile plants gave the ratio of 23 fertile to 32 sterile plants. These results pointed out that this spontaneous new mutation is inherited monogenically. Testcrosses between *msl*-Urbana and *Msl msl* unknown mutants confirmed our cytological observations of sterile plants. Sixteen F_1 plants had normal pollen, 15 F_1 plants were characterized by large, coenocytic pollen grains. This population gave a good fit to the expected 1:1 ratio, chi-square = 0.032, $P = 0.50-0.90$ (Table 1). Seeds of these 15 F_1 fertile plants will be planted in 1986 for further observations.

The results indicated that this mutation occurred independently and a single locus was conditioning male sterility. The gene responsible for male sterility is allelic to the *msl* locus.

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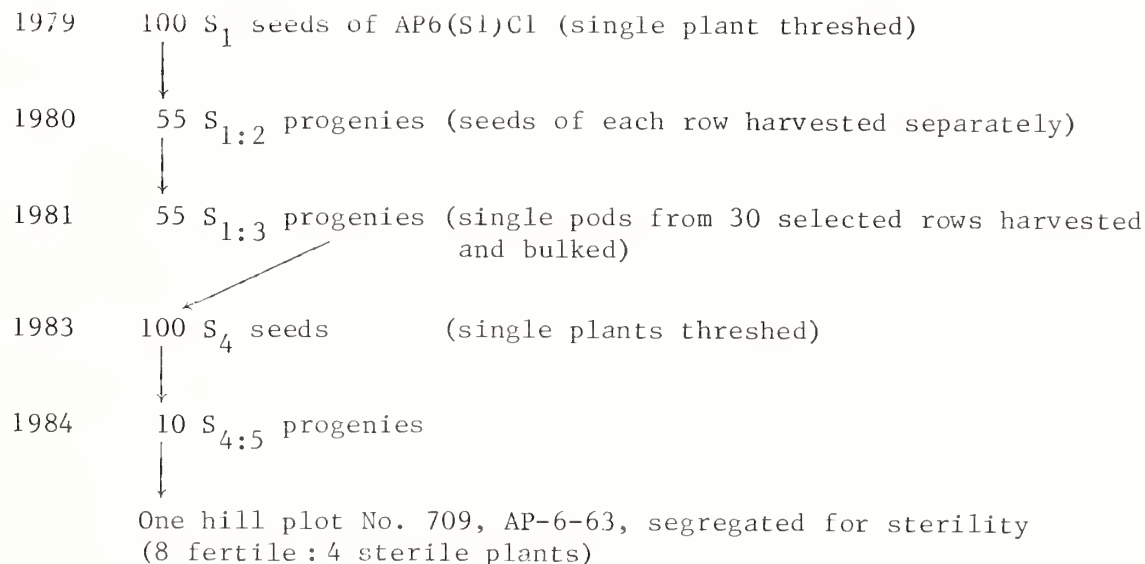


Figure 1. Origin of unknown sterile mutant

Table 1. Segregation ratios for fertility/sterility in $S_{5:6}$ progenies and F_1 testcross population

Parentage	Number of plants			Expected ratio	χ^2	P
	Observed	Fertile	Sterile			
$S_{5:6}$ progenies of fertile plants	532	392	140	3:1	0.4912	0.10-0.50
$S_{5:6}$ progenies of sterile plants	55	23	32			
F_1 (<i>msl msl</i> -Urbana) x <i>Msl msl</i> unknown mutant	31	16	15	1:1	0.032	0.50-0.90

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28 Test for apomixis in *ms4* male-sterile soybean.

Soybean plants homozygous for the male-sterile mutation *ms4* are capable of seed production in the absence of insect pollinators (Graybosch and Palmer, 1984). Cytological investigations have demonstrated the genesis of pollen grains by male-sterile plants at a frequency of 3.3% (Graybosch and Palmer, 1985). Pollen formed is identical to that of male-fertile plants, and will germinate when placed in an *in vitro* germination medium. A test using the genetic marker *y11* was designed to determine whether seed production by male-sterile plants was a function of the activity of these pollen grains, or apomixis. The *ms4* and *ms1* mutations both influence the process of postmeiotic cytokinesis during microsporogenesis. The *ms1* mutation also has a pleiotropic effect on female reproduction. A high frequency of polyembryonic and polyploid progeny results from the occasional omission of postmeiotic cytokinesis during megasporogenesis (Kennell and Horner, 1985). Since *ms1* and *ms4* demonstrate similar effects on male reproduction, it seemed possible that *ms4* also might influence female reproduction. Omission of cytokinesis during megasporogenesis could result in the formation of diploid eggs, followed by apomictic seed development. However, the recovery of polyploid and/or polyembryonic seedlings from *ms4* male-sterile plants has not been reported.

Male-sterile plants (*ms4 ms4 Y11 Y11*) were crossed with male-fertile plants heterozygous for *y11*. *y11* is a chlorophyll-deficient mutant; individuals heterozygous for *y11* display a yellow-green phenotype. Homozygosity for the recessive *y11* is a lethal condition. In the F_1 , male-fertile plants heterozygous for *y11* were selected and increased. F_2 seed was sown in single-plant progeny rows in the field in 1984 at Ames, Iowa. The F_2 population was rogued so that only individuals of the genotype *ms4 ms4 Y11 y11* remained. Seed production by these male-sterile plants was low, so F_3 seed was bulked for analysis. The F_3 was planted in 1985 at St. Charles, Missouri. Plants were classified for male sterility/fertility and for *y11*.

Seed produced by the F_2 male-sterile plants could have been the result of either self-perpetuation (self-pollination or apomixis) or outcrossing. Since fertile sibs were rogued from the F_2 , no male-fertile heterozygotes were available as donors of gametes carrying *ms4*. Thus, male-fertile individuals in the F_3 were the result of outcrossing; male-sterile plants only could have arisen via self-perpetuation. The classification of F_3 male-sterile plants

for *y11* is given in Table 1. If apomixis had occurred, all male-sterile individuals of the F_3 would have been of the genotype *Y11 y11*. If male-sterile progeny of male-sterile plants were the result of self-pollination, the resulting F_3 would have been composed of a population consisting of *1Y11 Y11:2Y11 y11:1y11 y11*. Since the *y11 y11* genotype is a seedling lethal, these plants could not be classified for male sterility. However, as the only sources of *y11* in the F_2 population were male-sterile plants, *y11 y11* individuals in the F_3 should have been of the genotype *ms4 ms4*. If *y11 y11* individuals are removed from consideration, self-pollination would be indicated by a 1:2 ratio of *Y11 Y11:Y11 y11*. Two chi-square analyses are given. Both fit the ratios expected if male-sterile progeny were the result of self-pollination.

Thus, the occurrence of apomixis is not supported by the results of this experiment. The test does demonstrate that the pollen grains formed by *ms4* male-sterile plants are capable of fertilization. There is no other explanation for the recovery of homozygous (*Y11 Y11* and *y11 y11*) individuals from male-sterile plants heterozygous for *y11*.

Table 1. Classification of F_3 male-sterile plants for the genetic marker *y11*

Genotype	N	Chi-square (1:2:1)	P	Chi-square (1:2)	P
<i>Y11 Y11</i>	79	2.786	>0.25	1.47	>0.10
<i>Y11 y11</i>	136				
<i>y11 y11</i>	60				

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3) ²⁴⁵ Linkage tests with a locus conditioning ineffective nodulation response to *Rhizobium fredii*.

A single Mendelian locus has been described (Devine, 1984) that conditions ineffective vs. effective nodulation response upon inoculation of soybean lines with *Rhizobium fredii* (Scholla and Elkan, 1984). A formal gene symbol has not been assigned to this locus; for convenience, we will refer to it here as Rj?. In a breeding program with a long-term goal of developing adapted cultivars with an effective response to improved *R. fredii* strains, it might be more efficient to select for the effective nodulation response indirectly (via a tightly linked genetic marker) than by screening lines for nodulation response directly. In this study, we tested 5 loci for linkage with the locus conditioning effective nodulation.

The cross 'Evans' (ineffective, Rj? Rj?) x 'Peking' (effective, rj? rj?) was made at Ames in the summer of 1983. F₁ plants were grown during the winter in Puerto Rico and F₂ populations were grown at Ames in the summer of 1984. F₂ plants were classified for pubescence color (conditioned by the *T-t* gene pair) at maturity, then single-plant threshed to develop F₂ families. F₃ individuals were grown in growth boxes and inoculated with *R. fredii* strain USDA 193, as described elsewhere (Du Teau et al., 1986), to determine F₂ genotypes for the nodulation response locus (Rj? ____ vs. rj? rj?). Isozyme analyses were performed as described by Griffin and Palmer (nd). The enzymes and loci assayed were: amylase activity (*Sp1*); aconitase activity (*Aco4*,) (Griffin and Palmer, nd); diaphorase activity (*Dial*); superoxide dismutase activity (*Sod1*). The data are presented in Table 1. Chi square analyses of the data indicate no significant deviations due to linkage. We conclude that the effective nodulation locus (Rj?) is independent of the loci *Aco4*, *Dial*, *Sod1*, *Sp1*, and *T*.

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Table 1. Segregation of a nodulation response locus (Rj?) and 5 other loci in the cross Evans (Rj? *Aco4-c Dial sod1 Spl-a t*) x Peking (rj? *Aco4-b dial Sod1 Spl-b T*)

Rj? x	Expected proportion						Total	χ^2	df
	3	6	3	1	2	1			
<i>Aco4</i>	22	44	15	3	9	8	101	3.45	2
<i>Spl</i>	16	46	19	3	9	8	101	1.90	2
<i>dial</i>	27	33	19	3	12	5	99	3.42	2

Rj? x	Expected proportion				Total	χ^2	df
	9	3	3	1			
<i>Sod1</i>	61	20	13	7	101	0.69	1
<i>T</i>	61	20	19	1	101	2.43	1

Segregation of Rj?:

81 Rj?___ : 20 rj? rj?; (3:1) = 1.46

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4) Allelism tests of T218H and T225H.

Genetic type T218M was found in 'Illini' in 1952 at Urbana, IL. T218H was derived from T218M by crossing a yellow branch as male parent with Illini. The F_1 plants were green. Segregation in the F_2 gave 3 green:1 yellow lethal plants. F_2 green plants gave ratios of 1 nonsegregating:2 segregating progenies in the F_3 generation, confirming monogenic inheritance (Palmer, 1978, unpublished). The recessive allele is carried as the heterozygote in T218H.

Genetic type T225M was found in 'Lincoln' in Iowa before 1955. T225H was derived from T225M. In the growth chamber, a few weak yellow plants flowered and were used as male parents onto Lincoln as female parent. One hybrid plant was obtained. The F_1 plant was green and segregation in the F_2 gave 3 green:1 yellow lethal plants. Confirmation of inheritance was obtained in the F_3 generation. The recessive allele is carried as the heterozygote in T225H (Sheridan and Palmer, 1975).

The objective of this study was to test for allelism between T218H and T225H.

Results: Reciprocal crosses were made by using green plants of T218H and T225H. Self-pollinated seed of plants used as parents were planted in the sandbench to determine the genotype of the parents, i.e., AA or Aa .

Data of F_1 hybrid plants from crosses between two heterozygous parents are given in Table 1. Yellow plants were observed in the F_1 in a ratio of 3 green:1 yellow lethal plants.

The F_1 green plants were field grown in Ames and were threshed individually. About half of the seed from each F_1 plant were planted in the sandbench to determine segregation for green and yellow plants. The remaining seed were planted in the field the following summer and were classified for plant color. Data were combined (Table 1). Segregation of pubescence color in the F_2 confirmed the hybridity of the cross.

Among all F_2 families of the cross T225H x T218H, there were 14 segregating:5 nonsegregating families ($\chi^2_{2:1} = 0.43$; $P = 0.75-0.50$). In the reciprocal cross, there were 8 segregating:3 nonsegregating families ($\chi^2_{2:1} = 0.21$; $P = 0.75-0.50$).

Five plants from each field-grown F_2 entry were threshed individually and 50 seed per entry were planted in the sandbench and segregating families were classified for plant color (Table 3).

Table 1. Ratio of green:yellow F_1 plants from reciprocal crosses of known heterozygotes of T218H and T225H (field data)

<u>T218H x T225H</u>			
<u>Green</u>	<u>Yellow</u>	<u>Chi square (3:1)</u>	<u>P</u>
12	4	0.00	1.00
<u>T 225H x T218H</u>			
<u>Green</u>	<u>Yellow</u>	<u>Chi square (3:1)</u>	<u>P</u>
21	6	0.10	0.90-0.70

Table 2. Ratio of green:yellow F_2 plants from reciprocal crosses of known heterozygotes of T218H and T225H (greenhouse and field data combined)

<u>T218H x T225H</u>				
	<u>Green</u>	<u>Yellow</u>	<u>Chi-square (3:1)</u>	<u>P</u>
Totals	2059	636	17.70	
Pooled chi-square (1 df)			2.83	>0.10
Homogeneity chi-square (7 df)			14.87	>0.05
<u>T225H x T218H</u>				
	<u>Green</u>	<u>Yellow</u>	<u>Chi-square (3:1)</u>	<u>P</u>
Totals	3183	957	50.01	
Pooled chi-square (1 df)			7.84	>0.005
Homogeneity chi-square (13 df)			42.17	>0.005

Table 3. Ratio of green:yellow F_3 plants from reciprocal crosses of known heterozygotes of T218H x T225H (greenhouse data)

<u>T 218H x T225H</u>				
	<u>Green</u>	<u>Yellow</u>	<u>Chi-square (3:1)</u>	<u>P</u>
Totals	899	272	15.36	
Pooled chi square (1 df)			1.96	>0.20
Homogeneity chi-square (23 df)			13.40	>0.95
<u>T225H x T218H</u>				
	<u>Green</u>	<u>Yellow</u>	<u>Chi-square (3:1)</u>	<u>P</u>
Totals	1783	482	32.14	
Pooled chi-square (1 df)			16.72	>0.005
Homogeneity chi square (42 df)			15.42	>0.995

In the cross of T218H x T225H, the number of F_2 entries evaluated in the F_3 was 40. The number of segregating entries was 24:16 nonsegregating (χ^2 2:1 = 0.9; $P = 0.50-0.25$). In the reciprocal cross, the number of segregating entries was 43:26 nonsegregating (χ^2 2:1 = 0.73; $P = 0.5-0.25$).

Discussion: If T218H and T225H were allelic, one fourth of the F_1 plants would be yellow lethal. If these loci were nonallelic, all F_1 plants would be green. In Table 1, the data from reciprocal crosses show that one-fourth of the F_1 hybrid plants were lethal. This suggests that T218H and T225H are allelic.

The F_2 segregation indicated that two-thirds of the green F_1 plants were heterozygous and one-third homozygous dominant. Among segregating entries of the reciprocal crosses, a ratio of 3.24 green:1 yellow for T218H x T225H and 3.33 green:1 yellow for T225H x T218H was calculated. In both cross combinations, there was a deficiency of yellow plants.

The F_3 segregation also gave a 2:1 ratio for heterozygous:homozygous dominant genotypes. For 218H x T225H, we observed 3.31 green:1 yellow and for T225H x T218H, 3.70 green:1 yellow. Again, for both cross combinations, there was a deficiency of yellow plants.

In the reciprocal crosses in the F_2 and F_3 , we observed all green plants or segregation approximating 3 green:1 yellow. Furthermore, we never observed a 9 green:7 yellow, which would indicate two nonallelic loci.

The significant deviations from 3:1 within and among families of the reciprocal crosses has been noticed previously in crosses with T225H (Palmer, 1984).

We believe that these data confirm the allelism of these two mutants. The event(s) that produced the unstable allele in T218HM and T225M occurred in different cultivars and in different years. We conclude that they represent two independent events.

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5) An additional beta-amylase mobility variant conditioned by the *Spl* locus.

The *Spl* locus (Orf and Hymowitz, 1976; Gorman and Kiang, 1978) codes for beta-amylase (Hildebrand and Hymowitz, 1980). Two mobility variants and two null variants have been described (Orf and Hymowitz, 1976; Kiang, 1981). We have been conducting a survey of isoenzyme variability in the soybean germplasm collections. We assay beta-amylase activity on 10% acrylamide gels (Davis, 1964) to determine genotypes at the *Spl* locus. A recent plant introduction from China (PI 464918) was found to have a beta-amylase with mobility intermediate to those of the *Spl-a* and *Spl-b* alleles.

This new variant was tested in crosses with lines carrying either the *Spl-a* or *Spl-b* alleles. The data are presented in Table 1. Both populations segregated in a 1:2:1 ratio as tested by chi-square, indicating that the new variant is conditioned by an allele of the *Spl* locus. We designate the allele *Spl-c*. The relative mobility of the three alleles is: *Spl-a*, Rf=.27; *Spl-c*, Rf=.30; *Spl-b*, Rf=.33.

Table 1. Allelism tests of an additional beta-amylase mobility variant at the *Spl* locus

Cross	Generation	Classes			N	χ^2
		<u>a/a</u>	<u>a/c</u>	<u>c/c</u>		
'Evans' x PI 464918 a/a x c/c (includes reciprocal)	F ₂	120	186	104	410	4.75
PI 257430 x PI 464918 b/b x c/c	F ₂	25	62	29	116	0.83

PI 464918 came into the U.S. under the name 'Ji Ti 4' from Heilongjiang Province, The People's Republic of China. Three other PIs from the same collection, 464916 ('Ji Ti 2'), 464917 ('Ji Ti 3'), and 464919 ('Ji Ti 5') were assayed to determine their genotypes at the *Spl* locus. None had the *Spl-c* allele. Further, in our survey of approximately 1500 accessions in the soybean (*Glycine max*) and wild soybean (*G. soja*) germplasm collections, PI 464918 is the only accession determined to have the *Spl-c* allele. The 'Ji Ti' series are all improved cultivars. The absence of the *Spl-c* allele in any other accessions indicates that this is probably a relatively recent mutation at the *Spl* locus.

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6) Enhancing seed set in *Glycine falcata*.

Research using wild relatives of the soybean, such as *Glycine falcata* Benth., a native of Australia, has been hampered by an extremely low seed set under greenhouse conditions in the absence of pollinating vectors. A quick and efficient method of enhancing seed set in this species was developed in working with *Neonotonia verdcourtii*, a species from Africa formerly included in the genus *Glycine* (Isely et al., 1980). Conventional soybean crossing techniques among flowers of one plant were tedious and time-consuming, and did not produce many seeds.

We found that a tool with a rough tip served better than a sharp forceps to move pollen from flower to flower. Such a tool seems always to be at hand in dried petioles from fallen leaves. A slim stiff petiole inserted between the two keel petals and moved across the stamens gathers pollen. Moving from flower to flower, quickly rubbing this make-shift tool across the stamens, results in production of an abundance of seeds. No care is needed as to which flowers are treated; the procedure can go from branch to branch within the same plant or between plants. A ten-minute visit to the plants each day to treat the new flowers is sufficient to produce good seed set.

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7) Variation in pollen receptivity in artificial crosses of *msl*-Urbana line.

General characters associated with the soybean male-sterile *msl* gene have been described in a previous study (Chen et al., 1985). Among the four spontaneous and independent *msl* source populations (Palmer et al., 1978), the Urbana male-sterile (*msl*-Urbana) line was reported to have 1) higher female fertility (Boerma and Cooper, 1978), 2) lower percentage of ovule abortion (Kennell and Horner, 1985), and 3) higher percentage of pollen-tube germination in male-sterile anthers (Chen et al., 1986). However, no report has mentioned whether gynoecia of male-sterile plants would have the same receptivity as those of male-fertile plants, when fertile pollen was applied to the stigma of male-sterile plants.

In a study of the germination and growth of male-fertile pollen on gynoecia of male-fertile homozygous *Msl Msl*, male-fertile heterozygous *Msl msl*, and male-sterile homozygous *msl msl* plants, we used the *msl*-Urbana line. Gynoecia of male-sterile plants allowed the germination and growth of fertile pollen grains as well as those of male-fertile plants. Pollinations from fertile heterozygous plants onto fertile heterozygous gynoecia, however, resulted in a lower percentage of pollen-tube growth than did the other combinations (Chen, 1985). Further investigations during different growing seasons in greenhouse plantings were conducted. In this study, we report variation in pollen-tube germination and growth in gynoecia of artificial crosses with fertile pollen among the *msl*-Urbana progeny.

Materials and methods: Four greenhouse plantings, 1984 summer (1984 S), 1985 winter (1985 W), 1985 early summer (1985 SI), and 1985 middle summer (1985 SII) were grown.

A sibling male-fertile line not segregating for male sterility was used as the homozygous male-fertile *Msl Msl* (FH) plant source. Seeds obtained from male-sterile plants produced either male-fertile *Msl msl* (Fh) or male-sterile *msl msl* (SH) plants. Plants were classified as male fertile or male sterile at the beginning of flowering on the basis of pollen grain stainability with I₂KI. Different combinations of cross-pollinations were made among these three genotypes. Artificial crosses were made in all combinations during the same time period, but varied in number of crosses for each combination. Gynoecia were collected from each artificial crossing combination 24 hours

after pollination and fixed in FAA for 24 hours. Fixation, clearing procedure, and staining were the same as described by Chen et al. (1986). Observations were made by using light and fluorescence microscopy.

Results and discussion: Observations of pollen-tube growth could be grouped into three categories: normal pollen-tube growth, pollen-tube growth retarded or pollen tubes degenerated in stigma or style areas, or no observable pollen-tube growth. Percentage of gynoecia with normal pollen-tube growth became our primary interest because of its possible indication of fertilization. Types of crosses, as well as percentage of gynoecia with normal pollen-tube growth among different seasons of greenhouse plantings, are shown in Table 1. Variation in percentage of gynoecia with normal pollen-tube growth from season to season was noted. Although consistency in variation from cross to cross was not observed, Figures A-F indicate that variation from environment to environment in crosses of FH x FH vs. FH x Fh, and SH x FH vs. SH x Fh follow the same pattern (Figures A, B, E, and F). Nevertheless, crosses of Fh x FH vs. Fh x Fh (Figures C and D) did not show the same pattern as those of the others. Whether these results suggest a heterozygote effect on the female gynoecia for pollen receptivity is not known.

The results of the 1984 summer study indicated that male-fertile pollen grains germinated and grew readily in the style of the male-sterile plants. However, in the Fh x Fh cross, normal pollen-tube growth in the gynoecia was observed in only 54% of the artificial crosses. This compares with 88%, 91%, and 84% for the FH x FH, SH x FH, and SH x Fh crosses, respectively. A chi-square test among the FH x FH, Fh x Fh, SH x FH, and SH x Fh crosses indicated distribution of percentage of gynoecia with normal pollen-tube growth, pollen-tube degeneration, and no observable pollen-tube growth is significantly different at the 5% level. Most of the variation is contributed from the Fh x Fh crosses.

The artificial crossing study was repeated in winter 1985, early summer 1985, and middle summer 1985 to determine if there was any heterozygote effect on cross compatibility. Definite conclusions cannot be made from these studies. Nevertheless, from the overall data, equivalence or superiority of pollen from the FH plants, compared with that of the Fh plants, was noticed when different pollen sources were pollinated onto the gynoecia of the same genotype. This was noted from all crosses among environments, except the Fh x FH vs. Fh x Fh crosses in 1985 W (Table 1, underlined). The average

percentage of gynoecia with normal pollen-tube growth from all growing seasons varied from 73.0% to 57.2% with the sequential order $FH \times FH > Fh \times FH > SH \times FH > FH \times Fh > Fh \times Fh > SH \times Fh$ (Table 1). However, differences in percentage of gynoecia with normal pollen-tube growth are statistically non-significant in most cases. The success rate in hand pollination is known to vary from person to person and from environment to environment (Fehr, 1978). In our study, different cross combinations were made the same day with a varying number of crosses by the same person. Thus, if the differences in percentage of pollen-tube growth between the paired crosses (the same female genotype crossed with FH or Fh pollen) varied randomly, both positive and negative differences ($\times FH$ vs. $\times Fh$) should be expected with equal probability among these paired comparisons. As shown in Table 1, however, only one pair of crosses showed a negative difference (Table 1, underlined) whereas nine of the others showed no or positive differences. Differences in stigma and style receptivity have not been reported in soybean. In maize and other species, gamete competition between self-pollination and cross-pollination has been addressed (Johnson and Mulcahy, 1978; Yamada and Murakami, 1983; Ottaviano et al., 1983; Currah, 1983; Sarr et al., 1983). In our study, variation from cross to cross was noted. From the combined data, it seemed that $FH \times FH$ had the highest average percentage (73.0%) of pollen-tube growth, while that of the $SH \times Fh$ had the lowest (57.2%). An average of 9% difference in percentage of pollen-tube growth between pollen from FH plants and Fh plants was observed in gynoecia of the same female genotype. Although variation observed in our study was not supported by statistical analysis, there is a general trend. Furthermore, the environmental effect on expression of pollen-tube growth in gynoecia was significant. Thus, variation in the percent of pollen-tube growth in gynoecia may be influenced by environmental factors, genotypes, or interaction of both. Sorrells and Bingham (1979) indicated that the *ms1* allele had an effect on microspore cytokinesis in some fertile *Ms1 ms1* F_1 plants. Whether the inconsistent results obtained in this study are due to the unstable expression of the *ms1* allele in the heterozygous condition is not known. Further research might clarify whether this variation is controlled by factors such as the compatibility for pollen-tube growth in gynoecia or the instability of the *ms1* allele.

Table 1. Percent of gynoecia with pollen-tube growth among crosses of *msl*-Urbana line grown in different environments

Environment ^b	Parental combinations ^a (♀ x ♂)						Average of crosses
	FH x FH	FH x Fh	Fh x FH	Fh x Fh	SH x FH	SH x Fh	
1984 S	87.5 ^c (24)	--	--	54.2 (24)	90.6 (32)	83.8 (37)	79.0 ± 8.4 (117)
1985 W	66.7 (21)	66.7 (21)	53.9 (39)	75.0 (32)	64.0 (25)	46.4 (28)	62.1 ± 4.2 (166)
1985 SI	52.0 (25)	50.0 (22)	68.8 (16)	38.8 (49)	41.4 (29)	27.3 (22)	46.4 ± 5.8 (163)
1985 SII	85.7 (63)	75.0 (60)	82.5 (57)	74.6 (55)	75.0 (44)	71.4 (56)	77.4 ± 2.2 (335)
Average of environments	73.0±8.4 (133)	63.9±7.4 (103)	68.4±8.3 (112)	60.6±8.8 (160)	67.8±10.4 (130)	57.2±12.8 (143)	65.1 ± 3.7 (781)

^aFH = Male-fertile homozygote, *Msl Msl*;
 Fh = Male-fertile heterozygote, *Msl msl*;
 SH = Male-sterile homozygote, *msl msl*.

^bS = summer; W = winter; SI = early summer; SII = middle summer.

^c() indicates total number of crosses.

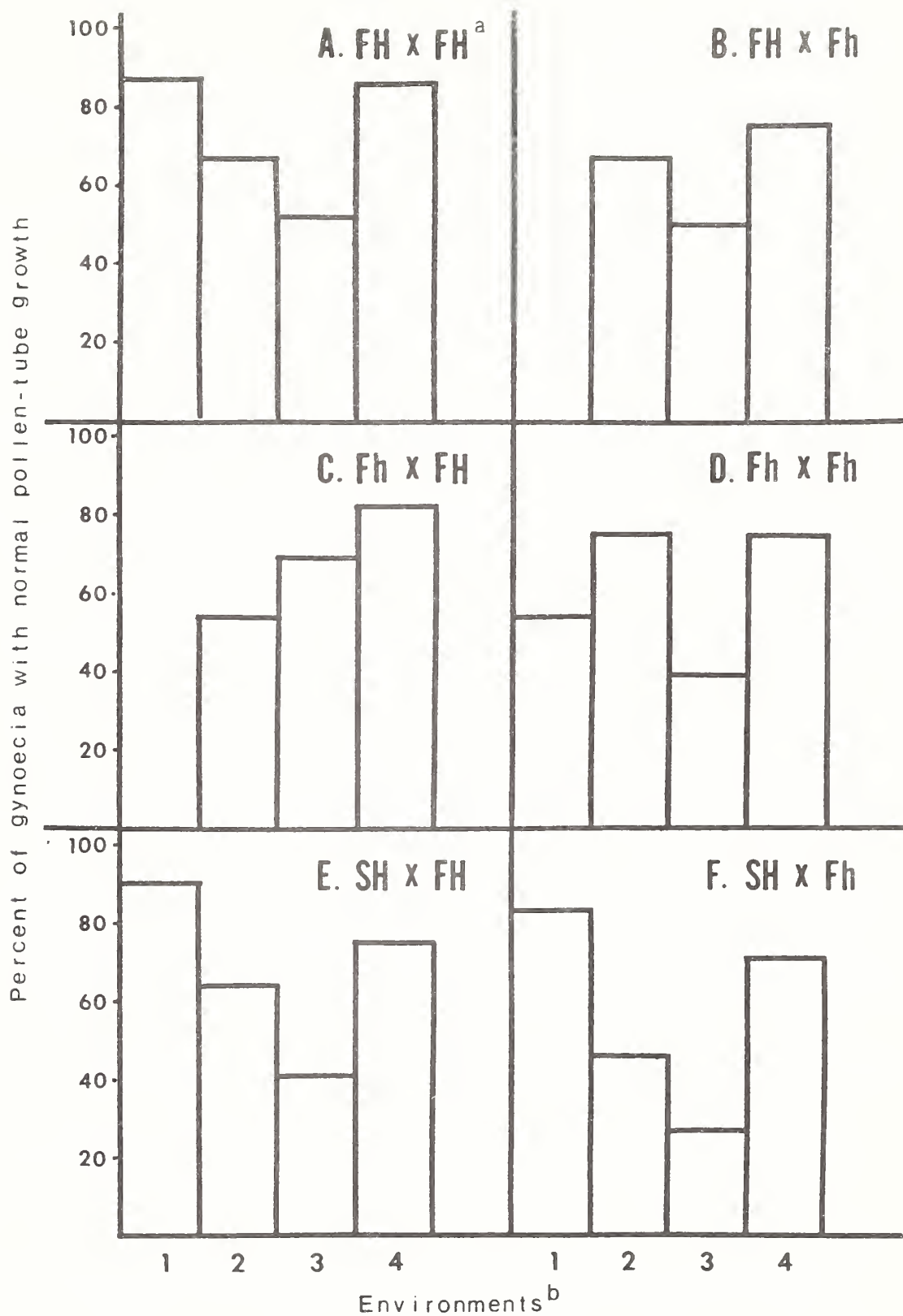


Fig. A-F: Percent of normal pollen-tube growth in gynoecia of artificial crosses of ms_1 -Urbana progeny among different environments of greenhouse plantings.

a: FH: Male-fertile homozygote; Fh: Male-fertile heterozygote; SH: Male-sterile homozygote

b: Number in each column indicates environments, 1: 1984 summer; 2: 1985 winter; 3: 1985 early summer; 4: 1985 middle summer

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1) Seed yield on field-grown ms_2 ms_2 male-sterile plants.

Seed set on male-sterile plants is of general interest to geneticists. For the quantitative geneticist, high seed set allows greater flexibility in the design of basic genetic experiments, including selection and variance component estimation studies. For the plant breeder, high seed set raises a hope of hybrid soybean production. Hybrid production, to be economical, requires adequate seed yield on male-sterile plants grown in the field.

Seed yield on male-sterile plants is often quite low in soybean. When grown in isolation in a greenhouse, seed set is almost absent for male-sterile plants, especially those conditioned by ms_1 , ms_2 , or ms_5 sources of sterility. Outside, however, seed set on male-sterile plants can be either high or low, depending on the specific ms gene, the micro-environment, and insect population involved.

For example, sterile plants conditioned by the North Carolina ms_1 gene have a seed set that is always a small fraction of normal (25% or less). Even when all environmental conditions are apparently satisfactory, the plant is not very receptive to pollination. Problems in megasporogenesis have been implicated (Cutter and Bingham, 1977). In contrast, male-sterile plants conditioned by the ms_2 gene can be pollinated more successfully in the open environment. Carter et al. (1983) compared seed yield on male-sterile and male-fertile plants grown outside in pots. Both high and low seed set on ms_2 male-sterile plants were observed. It was noted in that study that, when environmental conditions are ideal (including adequate pollen vectors), seed yield can be quite high on ms_2 male-sterile plants grown in pots. Seed yield was only 8% less than that of control plants in the two years tested.

We have occasionally observed high seed set on field-grown male-sterile plants when insect populations are high, insecticides are not used, and moisture, light, and temperature conditions are favorable. Few data are available to document the upper limit of seed set on ms_2 male-sterile plants in the field, however. In this communication, we report on seed yield of male-sterile plants grown in the field under conditions that we consider nearly ideal for cross-pollination.

Materials and methods: The general approach each year was to grow about 2000 plants segregating for ms_2 -conditioned male sterility in hill plots. Male-sterile plants were identified at flowering and then harvested individually at maturity. Seed yield was compared to the fertile control plants.

Genotypes: A randomly mating population segregating for male sterility was employed in this study. The population was developed in Raleigh, NC, by back-crossing the ms_2 gene twice into eight cultivars and lines: 'Gasoy 17', 'Jeff', 'Ransom', 'Johnston', 'Davis', 'Duocrop', and N79-1304. The ms_2 source was provided by R. L. Bernard and was a maturity group III line. Two random intermating cycles were completed, and the seed from sterile plants were used as planting seed in 1984. Seed from sterile plants in 1984 were used as planting seed in 1985. The population segregated about 55% fertile: 45% sterile in 1985.

Environment: The half-acre site was isolated from other soybean fields by over two miles. Insect pressure is typically low in this field and no control of insect infestation was attempted. Post-emergent herbicides were applied as needed in both years. A minimum of 12 honeybee hives were placed near the field each year. Actual distance from hives to male-sterile plants ranged from 30 to 150 yards. Moisture was adequate during pollination in both years, but light intensity was considerably lower in 1985 because of extended cloud cover. Plants flowered in the month of August, and no dramatic decreases in temperature were observed during pollination. The site was considered to be nearly ideal for cross-pollination. Plants were grown in a hill plot arrangement on 19-inch centers. Male-sterile and male-fertile plants were distributed randomly over the field because of the genetically segregating nature of the male sterility.

Identification of sterile plants at flowering: In our visual identification procedure, we classified plants only on those days when we knew that fertiles were in fact shedding pollen. If a single flower on a plant shed pollen, the plant was tagged fertile. Up to five fresh flowers per plant were checked for pollen shedding. If no flowers shed pollen, the plant was tentatively marked as sterile. On a different day, putative steriles were checked closely for pollen shedding and morphology. If no evidence of fertility was found, then the plant was labeled male-sterile. When time permitted, male-steriles were tested on three different days.

Although a pollen-germination test may have proved somewhat more reliable than our visual inspections, such a test was impractical for the large number

of plants we screened. Realizing that visual inspection is subject to occasional misidentification of plants, we carefully followed the protocol above in both years. In 1985, we used additional methods in the field to confirm our identification of steriles. The anthers of male-sterile plants were examined by magnifying lens. When the identity of a plant was in doubt, a dissection microscope was employed; shrunken anthers devoid of pollen were classified as sterile. Occasionally, anthers were crushed and stained with I_2KI for a final determination. Fertile pollen grains stained a golden brown. Progeny tests were also conducted for plants grown in 1985. These tests consisted of growing progeny from sterile plants that had either white flowers or gray pubescence. Segregation for these traits was taken as evidence of seed set by hybridization. Progeny tests indicated that our error rate for identification of male steriles was about 5%.

Harvest: Individual plants were harvested by hand and threshed with either a Swanson or Brewer mechanical thresher. All plants in the progeny test were threshed with the Brewer electric thresher because cleanout of seed is superior and the chance of mixtures is quite small.

Results: Seed set on the $ms_2 ms_2$ male-sterile plants was quite high (Table 1). Sterile plants produced yields that were 85 and 76% of normal in 1984 and 1985, respectively. Seed on sterile plants were larger than those on fertile plants in general. The increase in seed size partially explains the tendency of male-sterile plants to yield higher than the human eye might predict. This is especially true for our study in 1985. In that year, sterile plants could be seen to have fewer pods than fertiles at maturity. Stems stayed green, and leaves were slow in senescing. We guessed that yield on sterile plants might be only one-third to one-half that of normal plants. Actual yield results indicated that our visual observations were inaccurate and that sterile plants yielded 76% of normal. In 1984, by contrast, pod set was very high on sterile plants, and it was quite apparent before harvest that yield on sterile plants would be nearly normal.

The results clearly show that male-sterile plants can produce seed yield high enough to suggest possibilities for F_1 hybrid seed production. Our growing environment was nearly ideal in this study. Adequate soil moisture and honeybee populations at flowering, high temperatures and high relative humidity all contributed to the seed yield we observed. Seed yield on steriles would probably have been even higher in 1985, except for extended cloud cover which tended to retard cross pollination.

Inferences from the data are limited somewhat, of course, regarding seed set in a commercial hybrid production system. Our genotypes were arranged randomly in hill plots, rather than in rows. In a commercial venture, male-sterile plants would likely be grown in pure stand with pollen sources grown in nearby rows. The full potential for seed yield in such a system is not known at present. No practical method has been reported for obtaining a pure stand of male-sterile plants that are also fully female-fertile. The *msp* gene has been used to develop a pure stand of male steriles, but we have noticed that female fertility is usually very low on *msp msp* male-sterile plants.

Even though seed production on sterile plants may be adequate for hybrid production, other problems remain. These additional barriers to hybrid seed production include 1) maintaining a proper production environment for cross pollination over a large area, 2) determining appropriate heterotic combinations, 3) obtaining a pure stand of male-sterile, female-fertile plants, and 4) developing economical quality control methods. At present, we maintain an open mind concerning the feasibility of F_1 hybrid production. Continued research may provide solutions to these latter problems.

Table 1. Yield and seed weight of Ms_2 male-sterile and male-fertile plants in Raleigh, NC, in 1984 and 1985

Genotype	Year of evaluation	Seed yield	Seed weight	n [§]
		(g/plant)	(g/100 seed)	
Ms_2 [†] _____	1984	67.2*	18.2*	212
ms_2 ms_2		57.6	21.2	274.
Ms_2 _____	1985	38.5*	15.2*	199
ms_2 ms_2		29.6	20.8	215
Ms_2 _____	combined	52.9* [‡]	16.7*	411
ms_2 ms_2		43.6	21.0	487

*Fertile and sterile genotypes significantly different in the 0.05 probability level.

[†] Ms_2 _____ = male fertile; ms_2 ms_2 = male sterile.

[‡]Each year given equal weight in average.

[§]Number of plants harvested.

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1) Characteristics of a soybean genotype resistant to *Phomopsis* seed decay.

The disease *Phomopsis* seed decay of soybeans is considered to be the major cause of low quality, poorly germinating seeds in most areas where this crop is grown. This disease is caused by a complex of fungi consisting of *Diaporthe phaseolorum* var. *sojae* (Dps), *D. phaseolorum* var. *caulivora* (Dpc), and *Phomopsis longicolla* (Pl). In addition, Dps and Pl cause pod and stem blight and Dpc causes stem canker of soybeans.

Our research has shown that the soybean genotype PI 417479 exhibits a high level of resistance to *Phomopsis* seed decay. The purpose of this paper is to describe morphological, agronomic and disease reaction characteristics of this genotype. Information contained in this paper was compiled from data obtained by the authors and the report: Evaluation of the USDA Soybean Germplasm Collection, published by the USDA, Urbana, Illinois (Nelson and Amdor, 1986).

PI 417479 was introduced into the World Soybean Germplasm Collection from Japan in 1977. It has purple flowers, gray appressed pubescence, yellow seed coat, buff hilum, determinate growth type, and is classified as a Maturity Group IV genotype. However, at Columbia, MO, it reached growth stage R8 (Fehr et al., 1971) about three days earlier than the Maturity Group III cultivar 'Williams 82'.

PI 417479 reached a mature plant height of 78 cm with a lodging score of 2.0 (1 = erect and 5 = prostrate) when planted in mid-May in Urbana, IL. Similar results were observed at Columbia, MO. This genotype shattered readily when grown at Columbia, MO. Similarly, when plants were rated for shattering two weeks after harvest maturity at Urbana, IL, it received a shattering score of 3.5 (10 to 25% of open pods).

In addition to exhibiting resistance to *Phomopsis* seed decay, PI 417479 shows resistance to race 2 of frogeye leafspot caused by *Cercospora sojae* Hara. It is also resistant to race 1 (the only race it has been tested against to date) of *Phytophthora megasperma* f. sp. *glycinea*, the causal organism of phytophthora rot. However, PI 417479 is susceptible to bacterial blight caused by *Pseudomonas syringae* pv. *glycinea* and powdery mildew caused by *Microsphaera diffusa* (Cke. & Pk.). It is also susceptible to bud blight caused by the tobacco ringspot virus.

PI 417479 has a 100-seed weight of approximately 19.5 g and has a high percentage of two-seeded pods. Yield of this genotype averaged 2290 kg/ha when grown at Urbana, IL, over a two-year period. This was substantially lower than 3,410 kg/ha produced by 'Douglas' grown under similar conditions. Special characteristics of this genotype are the presence of high levels of anthocyanins in pod tissues as plants approach physiological maturity and the presence of waxy globules on the surface of mature seed coats. Due to the presence of anthocyanins, pods have a dark purple color as they near growth stage R7. Several researchers (Bhaskaran et al., 1975; Jalali et al., 1976; Larson and Bussard, 1979) have postulated that these anthocyanins possess antimicrobial properties. Experiments are currently being conducted by our research group to determine if these compounds are responsible for the resistance to *Phomopsis* seed decay in PI 417479. The waxy globules present on the seed coat visually resemble those shown by Calero et al. (1981) to be on the seed coat of 'Cobb' soybeans. They found that these waxy globules are possibly associated with reduced water absorption. However, our observations have shown that seed of PI 417479 absorb water readily.

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1) Cytoplasm sources of soybean cultivars grown in the United States and Canada.

In a recent study of cytoplasmic diversity in the soybean, made by restriction endonuclease analysis, Sisson et al. (1978) and Shoemaker et al. (1986) reported that cytoplasmic uniformity exists among currently grown soybean cultivars. Available evidence suggests that the potential cytoplasmic vulnerability in soybeans is no less than that of most other crops. The identification of cytoplasm from different sources may be one way of preventing possible future disease epidemics. Cataloging the cytoplasm of existing soybean cultivars according to source would be a first step in identifying different cytoplasm.

This report is a listing of sources of cytoplasm of named cultivars in the United States and Canada as determined from traceable pedigrees. Data used in our study came from three sources, as follows: (1) Pedigree of soybean cultivars released in the United States and Canada (Hymowitz et al., 1977); (2) Registration of soybean cultivars (various authors) in Crop Science (1976-1982); and (3) the Uniform Soybean Test-Northern States (Wilcox and Knapp, 1979, 1980 and 1981). Also see Delannay et al. (1983) and Specht and Williams (1984).

The cytoplasm source of each soybean cultivar was obtained by tracing back through the cultivar's pedigree to the maternal ancestor or maternal population. Cultivars that came from the same maternal ancestors or maternal populations were considered to have the same cytoplasm source. Cytoplasm sources of soybean cultivars were classified into major and minor groups according to the total number of cultivars having each source; cytoplasm sources contributing to 10 or more cultivars were included in the major groups and those contributing to less than 10 cultivars are assigned to minor groups.

Cultivars that have never been reported as female parents of crosses or populations for reselection to generate one or more new cultivars, cultivars having uncertain pedigree, and cultivars released by private companies were not covered in this study.

Cytoplasm sources of named soybean cultivars in the United States and Canada: Apparently, there are six major cytoplasm sources in named soybean cultivars in the United States and Canada (Table 1), five from China and one from Japan. These have contributed cytoplasm to a total of 177 cultivars. Among them, 'Mandarin' ranked number one, contributing cytoplasm to 71 cultivars (40.1%). 'A. K.' and 'Mukden' were second and third in importance, the former contributing to 30 cultivars (16.9%) and the latter to 28 (15.8%). The 24 minor cytoplasm sources (Table 2) contributed to 53 cultivars with 'Roanoke' and 'Manitoba Brown' being the most prominent sources.

Cytoplasm sources of major soybean cultivars recently grown in the United States: Ten major cultivars, each with more than 2% of the acreage grown in the North Central states (1978), were traced back to only three cytoplasmic sources, i.e., Mandarin, A.K., and Mukden. All three cytoplasm sources originated in China (Table 3). The most dominant cytoplasm source is Mandarin, which contributed to 70% of the total major cultivars. These results strongly demonstrate the possibility of cytoplasmic vulnerability of major soybean cultivars in the North Central states. Nine major cultivars that together contributed to about 83% of the cultivated acreage in the South Central states were traced back to 4 different cytoplasm sources (Table 4). Three cytoplasm sources came from China and one from Japan. Among the 4 sources, A. K. and 'Dunfield' each contributed to 33% of the total number of cultivars appearing to be of major importance. These results indicate that cytoplasmic vulnerability of major soybean cultivars in the South Central states may be almost as serious as that of major cultivars in the North Central states.

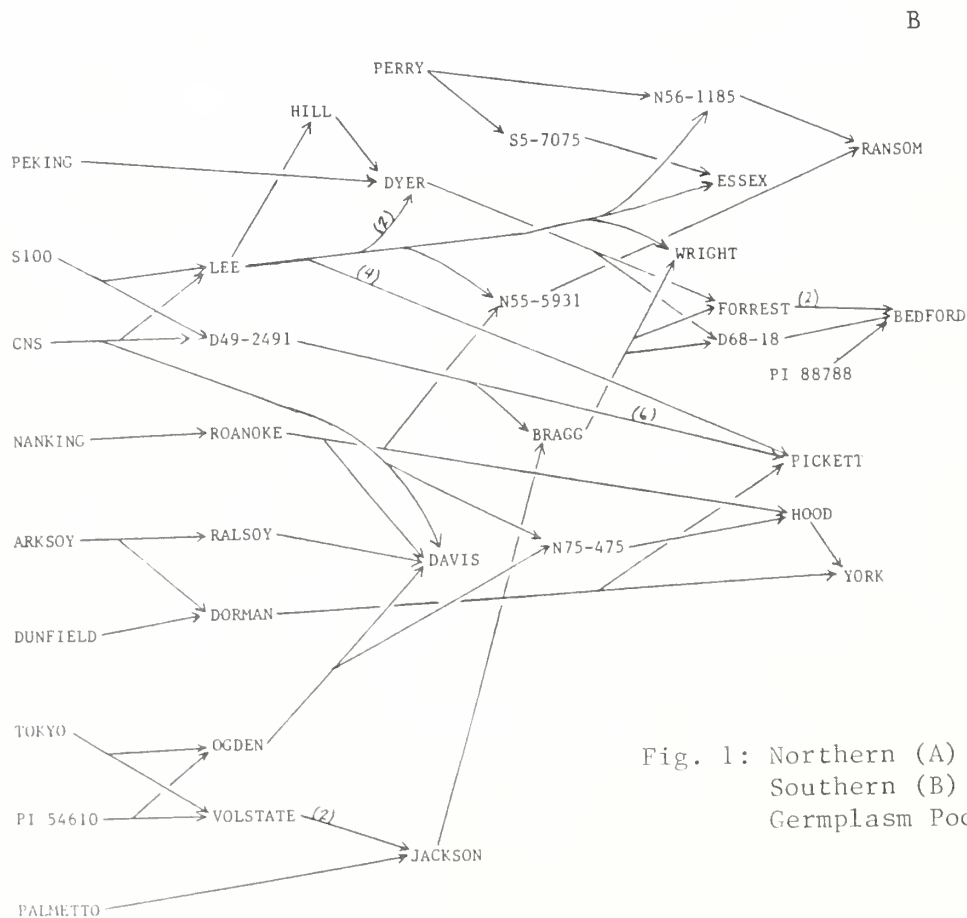
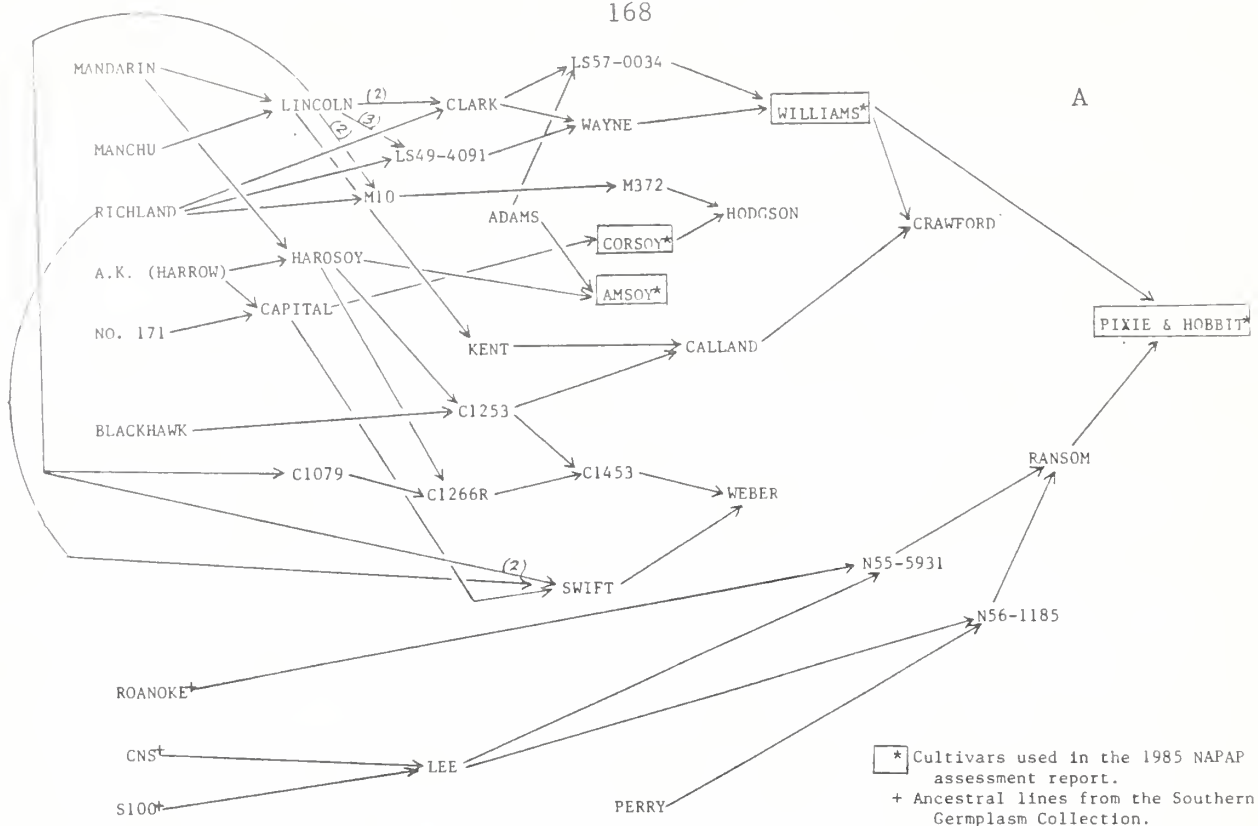


Fig. 1: Northern (A) and Southern (B) Soybean Germplasm Pools.

Table 1. Major cytoplasm sources of named soybean cultivars in the United States and Canada

Cytoplasm source [Origin]	Cultivars released		
	Number	%	Name
Mandarin (PI 36653) [NE China]	71	40.1	Aldelphia, Bonus, BSR 301, Chippewa, Chippewa 64, Clark, Clark 63, Columbus, Corsoy, Corsoy 79, Crawford, Cumberland, Cutler, Cutler 71, Desoto, Disoy, Douglas, Dunn, Elf, Ennis I, Fabulin, Fayette, Ford, Franklin, Gnome, Grant, Harcor, Har-dome, Harly, Harosoy, Harosoy 63, Hodgson, Hodgson 78, Hobbit, Kent, Lincoln, Lindarin, Lin-darin 63, Magna, Mandarin (Ottawa), Mandarin 507, Mead, Miles, Nebsoy, Oakland, Ottawa, Pella, Pixie, Pomona, Prize, Provar, Rampage, Renville, Roe, Shelby, Sloan, Sparks, Sprite, Swift, Tra-verse, Union, Vansoy, Vickery, Wayne, Weber, Wells, Wells II, Williams, Williams 79, Williams 82, Woodworth.
A.K. [China]	30	16.9	Adams, A.K. (FC 30761), A.K. (Harrow), A.K. (Kan-sas), Alamo, Amcor, Amsoy, Amsoy 71, Bossie, Cen-tennial, Chief, Curtis, Essex, HP-963, Illini, Jeff, Jupiter, Jupiter-R, Kino, Lee, Lee 68, Lee 74, Mack, Maple, Oksoy, Presto, Pickett, Pickett 71, S-100, Scott, Viking.
Mukden (PI 505230) [NE China]	28	15.8	Ada, Bavender Special, Bavender Special A, Baven-der Special B, Bavender Special C, Beeson, Beeson 80, Blackhawk, BSR 302, Calland, Century, Coles, Evans, Hark, Harlon, Hawkeye, Hawkeye 69, Law-rence, Madison, Merit, Monroe, Norchief, Protana, Ross, Simpson, Steele, Vinton, Vinton 81.
Manchu (PI 30593) [NE China]	18	10.2	Funman, Granger, Harman, Linman 533, Manchu (La-fayette), Manchu (Lafayette) B, Manchu (L55-143), Manchu (Madison), Manchu Hudson, Manchu Montreal, Manchu 2204, Manchu 3 Wisc., Manchu 606 Wisc., Manchukota, Mandell, Mansoy, Mingo, Scioto.
Tokyo (PI 8424) [Japan]	16	9.0	Bragg, Coker 338, Coker Hampton 266, Coker Hamp-ton 266A, Dortchsoy 31, Gasoy 17, Govan, Hampton, Hutton, Jackson, Majos, Ogden, Stuart, Tennessee Non-pop, Volstate, Wright.
Dunfield (PI 36846) [NE China]	14	7.9	Bay, Bedford, Carlin, Dare, Dorman, Dyer, Earlyana, Forrest, Hill, Nathan, Tracy, Tracy-M, Wabash, York.

Table 2. Minor cytoplasm sources of named soybean cultivars in the United States and Canada

Cytoplasm source	Origin	Cultivars released	
		Number	Name
Manitoba Brown	Unknown	8	Acme, Crest, Coment, McCall, Morsoy, Norman, Pagoda, Portage
Roanoke	China	7	Davis, Duocrop, Gail, Hardee, Hood, Hood 75, Ransom
Mammoth Yellow	Unknown	5	Dortchsoy 67, Hollybrook, Macoupin, Woods Yellow, Yelredo
Wilson (PI 19183)	China	4	Wilson B, Wilson 5, Wilson 5B, Wilson 6
Habaro (PI 20405)	USSR	3	Chestnut, Goldsoy, OAC 211
Korean	China	3	Anoka, Cypress No. 1, Grande.
Otootan	Taiwan	3	Avoyelles, Gatan, Tanner
Arksoy (PI 37335)	Korea	2	Ralsoy, Semmes.
Peking	China	2	Custer, Kingwa
No. 171	China	2	Capital, Clay
Willomi (PI 81044-1)	Japan	1	Willomi B
Nanda (PI 95727)	Korea	1	Yelnanda
Bansei	Japan	1	Bansei (Ames)
Clemson (PI 71569)	Japan	1	CNS
Aoda (PI 81043)	Japan	1	Verde
Cloud (PI 16790)	China	1	Sooty
Midwest (PI 6556)	China	1	Gibson
Patoka (PI 70218)	China	1	Perry
Norsoy	Unknown	1	Pridesoy 57
Haberlandt (PI 6396)	Korea	1	Hurrelbrink
Ebony (PI 6386)	Korea	1	Ilsoy
Jogun (PI 87615)	Korea	1	Jogun (Ames)
Kanro (PI 84928)	Korea	1	Kanrich
Sac (PI 80462)	Japan	1	Kim
Total		53	

Table 3. Cytoplasm sources of major[†] soybean cultivars grown in the North Central States (1978)

Cytoplasm source	Origin	Cultivars released			
		Number	%	Name	% of soybean acreage†
Mandarin	China	7	70	Williams	21.8
				Corsoy	11.8
				Wayne	5.5
				Woodworth	3.2
				Wells	3.1
				Hodgson	3.0
				Cutler 71	2.0
Total Mandarin					50.4
Mukden	China	2	20	Calland	3.8
				Beeson	3.0
Total Mukden					6.8
A.K.	China	1	10	Amsoy 71	5.9
Grand Total		10	--		63.1

[†]Grown on 2% or more of the soybean acreage.

[‡]Data from Bernard (1979).

Table 4. Cytoplasm sources of major[†] soybean cultivars grown in the South Central States (1978)

Cytoplasm source	Origin	Cultivars released		Name	% of soybean acreage [‡]
		Number	%		
A.K.	China	3	33.3	Lee	11.2
				Pickett 71	9.8
				Essex	7.2
Total A.K.					28.2
Dunfield	China	3	33.3	Forrest	18.7
				York	3.8
				Dare	3.0
Total Dunfield					25.5
Roanoke	China	2	22.2	Davis	10.2
				Ransom	3.3
Total Roanoke					13.5
Tokyo	Japan	1	11.1	Bragg	15.7
Grand Total		9			82.9

[†]Grown on 3% or more of the soybean acreage.

[‡]Data from Bernard (1979).

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1) Measured and predicted yield response of soybeans to simulated acid rain.

Modern soybean cultivars in the U.S. are highly related within the northern and within the southern maturity groups and they trace their genetic constitution to a small number of ancestral lines. On the other hand, there is much less genetic relationship between northern cultivars and southern cultivars. Examples of this can be seen in Figure 1, which shows the ancestral relationships among selected lines and cultivars developed from the northern and southern germplasm pools, respectively. Slightly more than 80% of the northern cultivars released during 1971-81 trace their genetic makeup to 10 accessions (Delannay et al., 1983). 'Mandarin', alone, accounts for more than 30% of the genes in the northern cultivar gene pool. Similarly, more than 80% of the genes in southern cultivars released during 1971-81 come from seven accessions. According to Delannay et al. (1983), CNS and S100 have contributed more than 50% of the genes in the southern cultivar gene pool. This narrow genetic base is a major concern to the breeders and geneticists due to vulnerability to diseases, insects, etc. On the other hand, the narrowness of the genetic base facilitates the assessment of future progenies' reactions to environmental changes. We are attempting to predict the response of soybean lines to acid rain on the basis of the reaction of the ancestral lines to acid rain.

Current knowledge concerning soybean response to acid precipitation is inconclusive in that stimulation, inhibition, or no effect on yield has been reported (Evans and Thompson, 1984; Evans et al., 1981; Heagle et al., 1983; Irving and Miller, 1981; Troiano et al., 1983). This uncertainty in response might be due to the differing growing conditions. Soybeans grown under optimum conditions might tend to overcome adverse effects of acid precipitation whereas stressful growing conditions might adversely affect productivity.

The objectives of our research were to evaluate: (1) yield response of ancestral lines and cultivars derived from them to Simulated Acid Rain (SAR); (2) interaction between environments and SAR for yield; and (3) predicted yield response to SAR of progeny from matings among ancestral lines.

Materials and methods: During 1985, the experiments were conducted at Knoxville and Milan, Tennessee. At each location, the 72 treatment combinations (optimum vs. sub-optimum soil fertility, three levels of SAR acidity, and 12 entries) were grown in a split-split strip block arrangement with three replications. The two soil fertility levels served as main strips, the three SAR treatments (pH 2.8, pH 3.2, and pH 4.3) served as the split-block and 12 entries served as the split-split block. The results of soil test were as follows: water pH of 5.9; buffer pH of 7.7; 46 kg/h P205; and 80 kg/h K20. In order to create two types of growing environments, lime (5.6 mt/h ground limestone) and fertilizer (89.6 kg/h P205 and 179.3 kg/h K20) were incorporated into the optimum strips to raise their fertility and soil pH to optimum levels. The sub-optimum strips did not receive any lime or fertilizer. Each experimental unit consisted of three rows 3 m in length with 0.9 m space between the rows.

The entries included eight ancestral lines ('AK Harrow', 'CNS', 'Manchu', 'Mandarin', PI 54610, 'Richland', S 100, and 'Tokyo') and four cultivars ('Amsoy 71', 'Essex', 'Lee 74' and 'Williams 82'). The SAR treatments were applied (spray-until-runoff) three times a week at Knoxville and two times a week at Milan from V2 until R7 stage. The amount of SAR represents mean weekly amounts of ambient rain based on the 30-year mean. The SAR solutions were made using the composition of rainfall as reported by Cogbill and Likens, a 1:1 mix of nitric and sulphuric acids substantiated with ammonium sulfate, calcium sulfate, sodium sulfate, potassium sulfate, and magnesium sulfate. The SAR was applied with a tractor-mounted sprayer at a pressure of 0.7 kg/sq cm using a PTO-driven diaphragm pump. The SAR quality was maintained by analysis of time of application samples for pH and other parameters.

The entries were hand-harvested and threshed in a plot thresher and their yields were recorded. The data were analyzed using SAS procedures (SAS Institute, Inc., Box 8000, Cary, North Carolina 27511-8000). The yields of four cultivars (Amsoy 71, Essex, Lee 74, and Williams 82) were predicted from ancestral lines' yield response and the covariance relationships among ancestral lines and these cultivars by using mixed models procedure (Henderson, 1975; Hill and Rosenberger, 1985). The covariance matrix for relationship among ancestral lines and cultivars was generated by using 'PROC INBREED' procedure in SAS. The ratio of phenotypic variance to genetic variance (the heritability of yield in soybeans assumed to be .4) was superimposed on the covariance matrix. We used a generalized inverse of covariance matrix to

obtain Best Linear Unbiased Prediction (BLUP) for yield response of cultivars to different environments. The yield data of these cultivars was eliminated, one cultivar at a time, before obtaining the BLUP estimate. The BLUP estimates of yield were compared to the actual yield of these cultivars.

Results and discussion: There was significant interaction between locations, entries, soil fertility levels, and acidity levels of SAR. At both locations, there was significant interaction between entries, soil fertility levels, and acidity levels of SAR except between entries*soil fertility levels and soil fertility levels*acidity levels of SAR at Knoxville.

At Knoxville, an increase in the acidity of SAR from pH 4.3 to pH 2.8 significantly decreased the yield of Manchu (28.8%) at optimum soil fertility and significantly increased the yields of Mandarin (51.4%) and Tokyo (36.5%) at sub-optimum soil fertility (Table 1). At Milan, an increase in the acidity of SAR from pH 4.3 to pH 3.2 significantly increased the yield of AK Harrow (124.7%) and significantly decreased the yield of Amsoy 71 (9.8%) under optimum soil fertility and any further increase in the acidity of SAR did not have any significant effect. The increase in the acidity of SAR from pH 4.3 to pH 2.8 significantly increased the yields of Richland (171.3%) and Tokyo (22.5%) at optimum soil fertility.

The predicted and actual yields of four cultivars are presented in Table 2. The predicted yields of Essex, Lee 74, and Williams 82 were always lower than their actual yields in both locations. The predicted yields of Amsoy 71 were always higher than its actual yields except at pH 3.2 with optimum soil fertility at Knoxville. At Milan, the predicted yields of Amsoy 71 were either greater than or similar to its actual yields. Based on their genetic background, Essex, Lee 74, and Williams 82 were expected to yield lower than their actual yields, indicating that they were not detrimentally affected by the acid rain. On the other hand, Amsoy 71 did not yield as expected from its genetic background, indicating that it might be sensitive to acid rain.

The comparison of actual yields (Table 1) did not give conclusive results but still gives an indication that Amsoy 71 is sensitive to acid rain under some growing conditions. The parents of this cultivar (Figure 1) are Harosoy and Adams. The parents of Harosoy, AK Harrow and Mandarin, were not detrimentally affected by SAR (Table 1). Therefore, the sensitivity of Amsoy 71 apparently was not inherited from either AK Harrow or Mandarin. Since Adams

Table 1. Mean yield (g/plot) of eight ancestral soybean lines and four cultivars with three pH levels of simulated acid rain

Entry	Knoxville						Milan					
	Sub-optimum [†]			Optimum			Sub-optimum			Optimum		
	2.8 [‡]	3.2	4.3	2.8	3.2	4.3	2.8	3.2	4.3	2.8	3.2	4.3
AK Harrow	392a*	388a	391a	446a	417a	441a	253a	266a	222a	241ab	346a	154b
Amsoy 71 [§]	442a	428a	372a	593a	582a	575a	364a	370a	374a	392ab	378b	419a
CNS	399a	440a	455a	500a	398a	709a	288a	303a	291a	340a	338a	389a
Essex [§]	549a	735a	683a	831a	795a	821a	806a	619a	709a	831a	804a	659a
Lee 74 [§]	524a	568a	556a	694a	617a	561a	476a	586a	521a	635a	718a	679a
Manchu	474a	378a	409a	430b	468ab	604a	337a	276a	268a	368a	304a	277a
Mandarin	480a	366b	317b	526a	402a	426a	294a	291a	281a	288a	278a	224a
PI 54610	473a	421a	546a	689a	739a	667a	364a	374a	484a	461a	529a	459a
Richland	377a	366a	357a	512a	429a	467a	278a	230a	225a	293a	209ab	108b
SI00	--	--	--	--	--	--	438a	467a	390a	442a	449a	383a
Tokyo	864a	533b	633b	851a	588a	1043a	429a	428a	467a	604a	545ab	493b
Williams 82 [§]	536a	567a	609a	813a	819a	730a	580a	559a	588a	710a	643a	597a

[†] Levels of soil fertility.[‡] pH of simulated acid rain.[§] Cultivar.

* Comparison of means to be made within locations, within each fertility level and separately for each entry (for example, in case of AK Harrow, the yields of three pH levels under sub-optimum fertility in Knoxville can only be compared with each other). Means followed by same letters are not different according to Duncan's Multiple Range Test ($P=0.05$).

Table 2. Actual and predicted[†] yields (g/plot) of four soybean cultivars with three pH levels of simulated acid rain

Entry	pH Levels of simulated acid rain											
	pH 2.8			pH 3.2			pH 4.3					
	KES*		MES [#]	KES		MES	KES		MES			
	Sub [§]	Opt [¶]	Sub	Opt	Sub	Opt	Sub	Opt	Sub	Opt	Sub	Opt
Amsoy 71	442 [‡] (493)	593 (608)	364 (374)	392 (415)	428 (456)	582 (543)	370 (363)	378 (413)	372 (457)	575 (587)	374 (365)	419 (337)
Essex	549 (442)	831 (624)	806 (390)	831 (472)	735 (495)	795 (558)	619 (425)	804 (495)	683 (499)	821 (621)	709 (400)	659 (455)
Lee 74	524 (474)	694 (649)	476 (476)	635 (507)	568 (552)	617 (594)	586 (440)	718 (500)	556 (537)	561 (712)	521 (437)	679 (448)
Williams 82	536 (468)	813 (552)	580 (344)	710 (376)	567 (423)	819 (502)	559 (323)	643 (350)	609 (418)	730 (579)	588 (322)	597 (309)

* Knoxville Experiment Station.

[#] Milan Experiment Station.

[§] Sub-optimum soil fertility and pH.

[¶] Optimum soil fertility and pH.

was not included in this study, no definite statement can be made about its contribution to the sensitivity of Amsoy 71 but it remains a suspect. Adams and Manchú (another sensitive line) were involved in the pedigree of Williams 82, which was not detrimentally affected by SAR. It is possible that the contributions made by Mandarin and Richland to the pedigree of Williams 82 outweighed the sensitivity contributed by Manchú and/or Adams. Evans and Thompson (1984) also observed a decrease in the seed yield of Amsoy 71 with an increase in acidity of simulated acid rain. The actual yields of Amsoy 71 under optimum soil fertility conditions at Milan decreased with increasing acidity of SAR. The actual yields of Essex, Lee 74, and Williams 82 either increased with increasing acidity of SAR or were similar at all acidity levels.

The use of mixed models to predict the yields of future progeny seems quite worthwhile. It might be used successfully to predict the performance of future progeny under varying environmental conditions. This technique was compared with six other techniques by Hill and Rosenberger (1985) for estimating yields of lines included in a series of trials that did not contain all entries in equal numbers. They concluded that Best Linear Unbiased Prediction (BLUP) method was most desirable since it gave smallest prediction errors.

Besides yield, data on maturity and plant height were also recorded on all plots at both the locations. In addition, transpiration rate and stomatal resistance were recorded for AK Harrow, CNS, Essex, Mandarin, and Williams 82 at Knoxville. The effects of SAR on plant height and maturity were not significant. The transpiration rate of Essex decreased, whereas that of CNS increased with increasing pH of SAR.

The results from one year at two locations indicate that (1) Essex, Lee 74, and Williams 82 were not detrimentally affected by the acid rain; (2) Amsoy 71 seems to be sensitive to SAR at least under some growing conditions; (3) the growing environment seems to affect the response of soybean cultivars and lines to acid rain; and (4) the comparison of actual and predicted yields might be a useful criterion in assessing sensitivities of soybean lines and cultivars to acid rain.

Additional greenhouse (at Knoxville) and field experiments (at Knoxville and Milan, Tennessee) will be conducted during 1986 to further assess the impact of acid rain on soybean growth and yield.

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1) Genetic linkage information.

Descriptions of the genetic traits indicated by the gene symbols in Table 1 are given in the chapter on Qualitative Genetics in the Soybean Monograph (Bernard and Weiss, 1973). Recombination was calculated on F_2 data using the product method as described by Immer and Henderson (1943). All linkage combinations tested were found to follow independent assortment except the combination *ln* and *p2*. Weiss (1970) previously reported these loci to be linked with a recombination frequency of 26.4 ± 1.4 centimorgans. Our data confirm this.

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Table 1. Soybean linkage test

Cross	Genes	A	B	C	D	Sum	%R	S.E.	Phase
T173 x T256	f ln	160	47	44	19	270	45	4	C
PI 83945-4 x T145	f p1	207	54	51	24	336	42	4	C
PI 83945-4 x T31	f p2	278	105	100	31	514	47	3.4	R
Clark 63 Rj2 x PI 83945-4	f rj2	244	75	81	29	429	48	3	C
PI 83945-4 x Clark 63 Rj4	f rj4	229	71	82	25	407	50	4	C
T135 x PI 83945-4	f t	296	107	80	21	504	45	3.5	C
PI 83945-4 x T139	f t	418	106	98	34	656	54	2.8	R
Clark 63 Rj2 x PI 83945-4	f t	253	83	72	21	429	48	4	R
T173 x T256	f w1	98	52	36	12	198	I ⁺	6	C
PI 83945-4 x Clark 63 Rj4	f w1	230	70	81	26	407	49	4	C
Clark 63 Rj2 x PI 83945-4	f w1	227	85	98	19	429	I ⁺	4	C
PI 83945-4 x T139	f y3	392	132	99	33	656	50	2.9	R
T135 x PI 83945-4	f y9	304	99	80	21	504	47	3.4	R
T135 x PI 83945-4	f y9	253	87	72	24	436	50	4	R
PI 83945-4 x T161	f y10	248	82	102	24	456	45	4	R
Minsoy x T31	fr1 p2	345	106	107	37	595	52	3	R
T230 x T31	ln p2	178	62	55	2	297	22	5	C
T31 x T135	ln p2	299	66	32	42	439	27	3	C
T41 x Hill	ln rj4	205	59	55	10	329	55	4	C
T41 x T256	ln w1	157	61	57	22	297	50	4	C
T173 x T256	ln w1	89	49	45	14	197	I ⁺	6	C
T31 x T135	ln w1	135	45	46	18	244	52	5	R
T135 x T109	ln y9	171	45	52	14	282	50	4	R
T31 x T135	ln y9	196	101	65	18	380	41	4	R
T230 x T31	ln y13	211	29	49	8	297	52	4	R
Clark 63 Rj2 x T145	p1 rj2	102	41	28	6	177	41	6	R
Clark 63 Rj2 x T145	p1 rj2	224	81	86	30	421	49	4	R
T145 x T230	p1 w1	341	146	142	43	672	45	3.1	R
Clark 63 Rj2 x T145	p1 w1	236	83	74	28	421	51	4	R
Clark 63 Rj2 x T145	p1 w1	111	32	26	8	177	51	6	R

Table 1. Continued

Cross	Genes	A	B	C	D	Sum	%R	S.E.	Phase
T139 x T145	p1 y3	355	126	89	25	595	53	3.2	C
T145 x T161	p1 y10	641	168	193	72	1074	45	2.2	C
T161 x T145	p1 y10	258	77	93	31	459	48	3	C
T145 x T230	p1 y13	344	143	145	40	672	55	3	C
T31 x T135	p2 w1	145	50	35	14	244	52	5	R
T31 x T135	p2 y9	178	60	50	15	303	48	4	R
T31 x T135	p2 y9	206	62	71	12	351	42	4	R
T31 x T161	p2 y10	403	116	148	38	705	48	2.9	R
T230 x T31	p2 y13	233	88	77	19	417	44	4	R
T230 x T31	p2 y13	240	73	61	23	397	53	4	R
Clark rj1 x T136	rj1 y6	246	68	88	29	431	52	4	R
T135 x Clark rj1	rj1 y9	136	42	48	8	234	41	5	R
T135 x Clark rj1	rj1 y9	169	45	65	14	293	47	4	R
T135 x Clark rj1	rj1 y9	184	55	60	23	322	53	4	R
Clark rj1 x T161	rj1 y10	294	72	106	27	499	51	3.3	R
T230 x Clark rj1	rj1 y13	219	117	63	34	533	50	3.6	R
Clark 63 Rj2 x PI 83945-4	rj2 t	253	66	83	27	429	53	3	R
Clark 63 Rj2 x T145	rj2 w1	237	68	82	34	421	45	3	C
Clark 63 Rj2 x T145	rj2 w1	99	31	38	9	177	54	6	C
Clark 63 Rj2 x PI 83945-4	rj2 w1	232	87	80	30	429	49	4	C
PI 83945-4 x Clark 63 Rj4	rj4 w1	232	79	79	17	407	I [†]	4	C
T161 x Clark 63 Rj4	rj4 y10	124	53	42	15	234	52	5	C
Clark 63 Rj2 x PI 83945-4	t w1	239	97	73	20	429	44	4	R
PI 83945-4 x T139	t y3	384	107	132	33	656	52	2.9	C
T135 x PI 83945-4	t y9	280	104	96	24	504	55	3.5	C
T135 x T256	w1 y9	185	50	46	17	298	46 [†]	4	C
T31 x T135	w1 y9	147	56	33	8	244	I [†]	5	C
T31 x T135	w1 y9	101	45	27	7	180	I [†]	6	C
T145 x T230	w1 y13	343	140	146	43	672	45	3.1	R

[†] I = independent, percent recombination >55.

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Evaluation of soybean germplasm for stress tolerance and biological efficiency.

Objectives: To evaluate soybean germplasm and cultivars for stress tolerance toward:

a. Moisture Stress

(B. Kpoghomou and V. T. Sapra, Alabama A&M University, Alabama)

Seventeen soybean genotypes were screened in a laboratory and growth-chamber experiment for water-stress tolerance characteristics. Three osmotic concentrations (0, -0.3 and -0.5 MPa) were used in an 8-day germination test conducted in the laboratory at Alabama A&M University. The Promptness Index (PI) and Germination Stress Index (GSI) were calculated (Bouslama and Schapaugh, 1984). Following the germination test, seedlings of the 17 cultivars were grown hydroponically in Hoagland solution at 0, -0.3, and -0.5 MPa. Twenty-four days after the treatments were applied, measurements on plant height, dry weight, and leaf water potential were recorded. The results showed that osmotic stress significantly affected the germination and genotypic variability among the cultivars. 'Lee', 'Wright', and 'Braxton' were most tolerant and 'RA401' and 'Bay' were most sensitive cultivars. Similar results were obtained in the seedling test. However, the germination (Table 1) test was more sensitive to osmotic stress than the seedling test.

(Bharat P. Singh, Fort Valley State College, Georgia)

Thirty soybean genotypes were screened in the greenhouse for moisture stress tolerance. Four genotypes (PI 324068, 'Coker 237', 123440, and 159322) were identified as most tolerant and three (PI 423911, AM-1007, and 416893) as least tolerant genotypes. The diffusive resistance and transpiration of the different genotypes at the time of wilting appeared to be similar. In the attached table, days taken for wilting under water stress by different soybean genotypes and their diffusive resistance and transpiration at the wilting stage are presented (Table 2).

Table 1. Germination stress indices of 17 soybean cultivars

Varieties	Means
Lee 74	63.59 ^a
Wright	61.09 ^{ab}
Braxton	60.99 ^{ab}
Davis	60.54 ^{ab}
Bragg	55.22 ^{abc}
Essex	54.77 ^{abc}
Centennial	53.87 ^{abc}
Bedford	52.78 ^{abc}
Forrest	49.08 ^{abcd}
Tracy	46.25 ^{bcde}
McNair 600	42.38 ^{cde}
Foster	41.93 ^{cdef}
Greenseed	37.60 ^{defg}
Hutton	32.81 ^{efg}
Stevens	29.17 ^{fgh}
RA 401	26.74 ^{gh}
Bay	18.70 ^h

MSE = 163.857.

Table 2. Days taken for wilting under water stress by different soybean genotypes and their diffusive resistance, and transpiration at the wilting stage

Genotype	Days for wilting	Diffusive resistance (sec cm^{-1})	Transpiration ($\mu\text{g cm}^{-2} \text{s}^{-1}$)
X 3104	15.4	2.92	2.93
PI 416937	16.7	1.71	2.37
PI 423911	14.7	1.94	2.44
MD-80IL-21	15.1	1.61	2.16
Deltapine 506	18.0	1.28	2.07
PI 408039	18.2	1.66	1.90
VR 3393	18.7	1.52	1.43
Ms ₂ Ms ₂	17.2	1.42	1.96
PI 417063	17.8	1.26	2.35
X 4126	17.0	1.40	2.00
Peking	17.8	1.40	2.43
Burr	15.7	1.75	3.00
PI 80837	21.0	1.78	1.94
AM-1007	14.0	1.95	2.58
PI 339984	16.7	1.55	2.19
Classic	21.3	1.68	1.89
PI 171442	17.8	1.70	1.90
PI 381668	19.0	1.41	1.87
Am-1009	19.8	1.43	1.54
PI 159319	15.0	1.51	2.21
Deltapine 246	19.0	1.38	2.18
PI 324068	23.0	2.01	1.62
Cocker 237	23.5	2.71	1.92
PI 407868C	16.0	2.45	1.40
PI 416893	14.7	2.09	2.19
PI 85437	19.3	1.52	2.19
PI 417419	16.0	1.70	2.31
Haberlandt	17.5	2.23	1.90
PI 123440	23.0	1.56	1.61
PI 159322	23.2	1.91	1.71

b. Pests

(M. Rangappa and M. E. Kraemer, Virginia State University, Virginia)

Soybean maturity groups V, VI, VII, and VIII have been screened systematically and accessions possessing potential source of natural resistance to Mexican Bean Beetle (MBB) have been identified along with several highly susceptible accessions for future studies. About 75% of the germplasm of maturity groups III and IV has been screened initially in 1985. A detailed copy of the screened germplasm can be obtained from scientists at Virginia State University.

Also, about 80 genotypes identified as resistant to several factors of stress tolerance and biological efficiency by other participating institutions of the project were planted at Virginia State University Research Station and evaluated for MBB resistance. Ample seed stocks of each accession were recovered for future studies.

The mechanisms of soybean resistance to the MBB are also being investigated by scientists at Virginia State University. Trypsin inhibitory activity (TIA) was found in the leaves of soybeans. Although TIA has been reported from other leguminous species, this is the first report from soybean leaves. The quantity of TIA increased with increasing plant age and MBB defoliation, and relatively large quantities were present in mature leaves (150-600 μ g trypsin inhibited per g leaf). Although there was no evidence that TIA affects MBB soybean preference, it is probable that TIA increases soybean antibiosis during a critical stage in the life cycle of the MBB, i.e., preparation for adult overwintering. Also, preliminary work has been done on ultrastructural differences in cell wall, cuticle thickness, and wax-layers of selected soybean leaves using electron microscopic techniques to establish mechanisms of resistance.

c. Harvest Index

(A. Bhagsari, Fort Valley State College, Georgia)

Simultaneous investigations were conducted at experiment farms at Fort Valley State College and Maryland Eastern Shore in 1985 with 42 soybean genotypes (14 each from MG III, IV, and V) to determine seed yield efficiency (SYE) and grain yield and their relationship to other agronomic traits. The mean seed yield efficiency ranged from 34 to 51, 35 to 50, and 28 to 59% for MG III, IV, and V, respectively. The mean grain yield for three MGs was similar and ranged from 19.65 (MG III) to 22.86 (MG V) quintals/ha. On 25 July 1985,

mean leaf area index (LAI) was 3.94, 5.24, and 5.02 for MG III, IV, and V, respectively, and LAI declined for all three groups at the next sampling date of August 15. The specific leaf weight (SLW) increased at successive samplings until the R7 stage. There was a wide range in SYE within each maturity group, but it was not related to grain yield. However, mean grain yield of two cultivars included in each of the three maturity groups was 34.6 and 43.1% higher than the mean for the groups (Tables 3-5).

Table 3. Seed yield efficiency, grain yield, leaf area index, and specific leaf weight of soybeans (Maturity Group III), 1985

Cultivar/PI	Seed yield efficiency (%)	Grain yield (quintals/ha)	<u>Leaf area index</u>		<u>Specific leaf weight</u>	
			July 25	Aug. 15	July 25	Aug. 15
PI 79628	51.42	14.80	3.01	1.62	3.38	3.90
Williams-82	49.68	28.67	3.85	3.16	3.58	4.06
Williams	47.93	24.20	3.01	2.71	3.64	3.40
BSR.301	46.85	25.00	4.18	1.94	3.42	4.03
PI 54615-1	46.25	19.11	3.64	1.43	3.43	3.69
PI 84957	45.47	16.71	3.95	1.09	2.93	3.56
PI 57334	44.20	18.62	5.60	2.57	3.25	3.21
PI 70189	43.93	16.91	3.15	1.61	3.72	3.64
PI 54610-1	41.85	27.07	4.82	3.27	3.34	3.95
PI 68479-1	39.50	13.64	4.03	1.28	3.87	3.96
PI 54583	38.40	12.80	3.45	2.22	3.83	3.97
PI 68398	37.55	28.73	3.80	2.88	3.54	3.35
PI 80841	35.50	12.60	4.48	1.43	3.12	3.20
PI 62202	33.61	16.24	4.17	1.39	3.38	3.17
Mean	43.01	19.65	3.94	2.04	3.49	3.65
LSD (0.05)	10.22	14.22	1.93	1.67	0.52	0.99

Table 4. Seed yield efficiency, grain yield, leaf area index, and specific leaf weight of soybeans (Maturity Group IV), 1985

Cultivar/PI	Seed yield efficiency (%)	Grain yield (quintals/ha)	Leaf area index		Specific leaf weight	
			July 25	Aug. 15	July 25	Aug. 15
PI 82264	49.56	23.38	7.38	5.45	2.74	3.09
PI 83891	46.95	23.82	5.24	4.17	3.24	3.21
PI 86103	45.79	24.27	5.52	4.14	3.24	2.89
PI 83889	45.54	20.60	4.17	3.39	3.12	4.01
PI 70242-2	45.25	23.27	6.43	3.33	2.92	3.60
PI 85469	44.65	21.51	6.62	3.66	3.06	3.75
PI 61947	43.31	21.02	3.68	3.76	3.08	3.85
PI 19976-1	42.95	26.20	4.74	3.28	3.06	3.78
PI 84644	42.49	19.85	5.32	3.35	3.18	4.05
PI 84751	41.49	24.69	6.38	4.65	2.61	3.06
Douglas	41.29	33.56	4.42	4.87	2.18	3.30
Union	39.24	28.80	5.44	2.95	3.63	3.98
PI 63468	36.57	14.31	4.44	1.28	3.26	3.68
PI 60970	34.56	14.80	3.61	2.78	3.12	4.45
Mean	42.83	22.86	5.24	3.65	3.03	3.62
LSD (0.05)	12.78	11.19	2.61	2.19	0.59	0.73

Table 5. Seed yield efficiency, grain yield, leaf area index, and specific leaf weight of soybeans (Maturity Group V), 1985

Cultivar/PI	Seed yield efficiency (%)	Grain yield (quintals/ha)	Leaf area index			Specific leaf weight		
			July 25	Aug. 15	Sept. 3	July 25	Aug. 15	Sept. 3
PI 416447	59.23	25.29	4.65	4.79	2.03	3.39	3.45	3.61
PI 416838	49.29	29.38	7.04	6.07	3.38	2.86	3.28	3.43
Forrest	44.87	37.31	6.58	6.15	3.84	3.12	3.69	4.04
PI 423762	42.27	14.04	6.36	4.19	1.61	3.16	3.67	3.71
PI 423799	40.83	16.76	4.04	4.96	2.77	3.06	3.45	3.25
PI 417141	39.54	18.45	5.72	3.86	1.87	3.02	3.67	4.01
PI 417356	38.31	16.42	3.14	1.49	1.07	3.79	3.97	2.92
PI 417493	37.82	16.36	4.00	3.48	1.44	3.48	3.68	3.42
PI 417090	37.19	20.00	4.10	4.08	1.44	2.67	2.81	6.25
PI 417494	36.95	20.53	4.48	3.80	2.95	2.89	3.14	3.12
PI 417418	34.80	18.89	4.50	3.75	3.33	3.86	4.08	4.42
PI 417172	34.76	15.51	3.75	3.91	1.47	3.41	3.43	3.10
PI 417337	34.13	14.75	5.81	4.21	2.18	3.27	3.23	3.59
Essex	27.72	20.85	6.11	6.11	6.48	2.63	3.12	3.37
Mean	39.84	20.32	5.02	4.35	2.56	3.19	3.48	3.73
LSD (0.05)	13.16	7.26	2.36	2.26	2.56	0.55	0.39	1.60

d. Micronutrients

(M. R. Reddy, North Carolina A & T, North Carolina)

A greenhouse experiment was conducted to evaluate the response of different soybean genotypes to manganese application. Twenty-five soybean genotypes belonging to different maturity groups were grown in a greenhouse using a Lynchburg sandy loam soil collected from Sampson County, NC. It is a coastal plain soil deficient in manganese. Manganese rates were 0, 15, and 30 kg per hectare. The experimental design was a split plot with three replications.

Results indicated differences in shoot weight among the genotypes tested due to manganese rates (Table 6). Genotypes (PI 96089, PI 279621, PI 423911, PI 417063, PI 417136, PI 423986, FC 31668, FC 31737, PI 416937, and L-76-0132) responded positively to manganese application and resulted in higher shoot weights. Some of the above genotypes gave favorable increase in shoot weight at 15 and 30 kg per hectare manganese, whereas others resulted in higher shoot weight at either 15 or 30 kg per hectare manganese. Genotypes 'Bedford', PI 230978, PI 417123, and PI 123440 responded negatively to manganese by giving a lower shoot weight than the control. There was no significant response by remainder of the genotypes to manganese addition. There was a significant increase in manganese concentration in leaf tissue of the genotypes (Table 7) as the rate of manganese increased. Relatively higher manganese concentration (30 kg/ha) in leaf of some genotypes resulted in poor plant growth and lower shoot weight.

e. Diseases

(R. P. Pacumbaba and V. T. Sapp, Alabama A&M University, Alabama)

Screening of improved soybean lines from Alabama A&M University for multiple resistance against bacterial blight, stem canker, and soybean cyst nematode in the greenhouse and in the field continued at Alabama A&M University. Lines obtained from Virginia State University in MG IV (PI 339984, PI 408039, PI 80837); MG V (PI 96089, PI 123440, PI L-76-0132, PI L-77-0049, 'Hill', 'Essex'); MG VI (FC 31665, PI 407868C, PI 159322, PI 416937, PI 379621, PI 221713, PI 230978, 'Lee'); MG VII (PI 423911, PI 229358); and MG VIII (PI 417134, PI 417063, PI 417061, PI 416893) were screened. Initial results indicated PI L-76-0049 is resistant to bacterial blight, PI 159322 and PI 230978 are resistant to soybean cyst nematode (race 3 and 5), and PI 417061 has multiple resistance to bacterial blight and stem canker. Other screened lines, viz., PI L-76-0132, PI 96089, PI 123440, PI 221713, and PI 417063, showed doubtful

resistance to bacterial blight, stem canker, and soybean cyst nematode. Further screening for resistance to these diseases will be continued.

Table 6. Effect of Mn rate on shoot weight of soybean genotypes

Soybean genotypes	Shoot weight (g/plant)		
	0 kg/ha Mn	15 kg/ha Mn	30 kg/ha Mn
FC 31665	2.3	2.8	3.5
FC 31737	2.2	3.0	3.2
PI 96089	2.2	3.3	3.0
PI 123440	3.6	2.9	2.2
PI 171442	2.8	3.3	2.7
PI 200506	3.3	3.2	3.0
PI 208788	3.2	3.2	3.6
PI 230978	3.1	3.2	1.7
PI 279621	1.2	3.0	1.8
PI 324924	3.0	3.3	2.9
PI 379618	2.2	2.1	2.4
PI 381668	2.1	2.4	2.3
PI 416900	2.3	2.9	2.5
PI 416937	2.2	2.5	2.8
PI 417063	2.4	2.6	2.8
PI 417123	3.0	2.8	2.7
PI 417136	2.3	2.8	2.9
PI 423911	2.4	2.7	3.7
PI 423986	2.8	2.7	3.4
L-76-0049	3.2	3.3	3.1
L-76-0132	2.3	2.6	2.9
Bedford	2.6	2.6	1.5
Cocker 237	2.9	3.2	2.7
Deltapine 506	2.5	3.5	2.8
Easy Cook	3.3	3.3	2.9

Table 7. Relationship between Mn rate and Mn concentration in soybean genotypes

Soybean genotypes	Leaf Mn ($\mu\text{g/g}$)		
	0 kg/ha Mn	15 kg/ha Mn	30 kg/ha Mn
FC 31665	29.7	36.0	52.3
FC 31737	24.2	25.7	43.3
PI 96089	25.8	26.8	37.0
PI 123440	30.2	33.2	43.7
PI 171442	26.5	34.0	59.5
PI 200506	26.7	24.8	53.5
PI 208788	25.7	24.3	40.2
PI 230978	19.0	25.0	55.5
PI 279621	15.3	21.3	39.5
PI 324924	24.0	24.7	50.5
PI 379618	28.8	28.0	52.3
PI 381668	28.3	27.0	46.3
PI 416900	20.8	26.5	51.0
PI 416937	21.5	25.3	43.8
PI 417063	29.2	24.8	45.3
PI 417123	27.8	27.0	58.7
PI 417136	24.0	28.5	49.8
PI 423911	25.8	23.3	55.5
PI 423986	23.7	27.0	48.0
L-76-0049	22.3	34.3	57.3
L-76-0132	24.8	34.5	43.0
Bedford	21.8	30.8	52.3
Cocker 237	33.7	40.8	66.0
Deltapine 506	26.2	30.3	67.7
Easy Cook	24.0	27.6	44.0

f. Nitrogen Fixation

(McArthur [Floyd, Alabama A&M University, Alabama])

Twenty-two soybean germplasm lines were grown in 1/5 Steinberg solution containing 6 ppm Al in 4L pots at pH 4.4 during the 1985 growing season to evaluate their tolerance to acidity and aluminum stresses. Plants were grown in three replications and separated on the basis of relative root lengths ratios (RRL = root length [cm] of plants grown in 6 ppm Al divided by root length [cm] of plants grown without Al). The system of classification was RRL >100% = highly tolerant; 85-99% = tolerant; 74-84% = sensitive; and <74% = highly sensitive. The data indicated ten lines (PIs 96089, 159322, 221713, 230978, 379621, 416937, 423986, 116893, FC 31665, and 'Deltapine 246') were highly tolerant; three lines (PIs 159319, 381668, and 'Deltapine 506') were tolerant. The sensitive lines were PI 324924, L-760132, and L-760049. Highly sensitive lines were PIs 123440, 324068, 417061, 417136, and 117258.

Twenty-one additional soybean germplasm lines were evaluated for their symbiotic performance with an acid tolerant rhizobium strain (USDA 110) at pH 4.4 in solution culture. Triplicate replications of plants were grown in the growth chamber in 4L black plastic pots containing N-free Fahreaus solution inoculated with USDA 110 rhizobium. Plants were harvested after 35 days. Nitrogenase activity ($\mu\text{mole C}_2\text{H}_4/\text{h/pl}$) ranged from 4.8 to 44.4. The lines with the highest nitrogenase activities were PI 423824 and FC 31737 with 44.0 and 44.4 $\mu\text{moles C}_2\text{H}_4/\text{h/pl}$, respectively.

Plants with nitrogenase activity greater than 30 $\mu\text{moles C}_2\text{H}_4/\text{h/pl}$ included PIs 70188, 80834-1, 423824, 97150, 181565, and FC 31737. Lines with nitrogenase activity ranging between 20-29 $\mu\text{moles C}_2\text{H}_4/\text{h/pl}$ were PIs 70013, 417135, 227557, 90768, and 423969.

g. Soil Acidity

(S. C. Tewari and P. W. Igbokwe, Alcorn State College, Mississippi)

Three years of field trials (1981-83) with six cultivars of soybeans ('Bedford', 'Bragg', 'Braxton', C-237, 'Forrest', and 'Tracy M') conducted on the Memphis silt loam soil showed greater resistance to low pH (5.0-5.5) for Forrest and Bedford as compared to the other cultivars. However, at pHs lower than 5.0, seed formation of all the cultivars was adversely affected, especially under moisture stresses. Greenhouse and laboratory studies during the same time period indicated higher P absorption for Forrest and Bedford at pH 5.0 to 5.5.

Two years of study (1984-85) with 12 and 19 cultivars in the field indicated little reduction in the Harvest Index with lower pHs for 'Ogden', 'Gassy', PI 324924, PI 90768, PI 89469, FC 31727, 'Ransom', 'Kirby', 'Centennial' and 'Foster' as compared with the other cultivars. In greenhouse and laboratory studies during the same time period, these cultivars were comparable to Bedford and Forrest in efficiency for absorbing P (more than 650 ppm). These same cultivars also absorbed less Al (less than 23 ppm) and may be considered as acid resistant at a pH of 5.0 and above when compared with the other cultivars tested. Out of a total of 34 cultivars evaluated in the greenhouse and in the laboratory, five cultivars ('Peking', PI 479491, 'Tracy M', PI 96089, and PI 123440) absorbed more than 23 ppm of Al from the soil at a pH of 5.5. These cultivars may be considered intermediate in acid tolerance at a pH of 5.5. The extractable Al and P in the soil at a pH of 5.5 was 1.5 ppm and 18.5 ppm, respectively. Further screening and testing of these promising genotypes are being conducted.

Reference

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1) Characteristics of soybean mutants, induced by chemical mutagens and gamma-rays.

Four varieties of soybean were developed in our country by using experimental mutations. Mutant varieties 'Universal' and 'Beregovchanka' were developed by direct selection of changed plants after mutagen treatment. 'Rannaya 10' and 'Volna' were created by combining hybridization and mutagenesis. Some prospective mutants created in All-Russian Institute of Soybean, All-Union Institute of Oil-Producing Crops and other research institutions are now in the National Soybean Variety Trial. These data demonstrate advantages of the method of creating initial material by mutagenesis, especially for those crops in which developing large quantities of hybrids is difficult.

In our investigations in 1975-1979, we studied mutagen activity of nitrosoethylurea (NEU), nitrosomethylurea (NMU), nitrosodimethylurea (NDMU), ethyleneimine (EI), ethylene oxide (EO), dimethylsulfate (DMS) and gamma-rays on a number of soybean varieties. NMU, EO, and DMS were tested in liquid and gaseous phases.

In experimental variants of M_2 , we selected about 1000 changed plants, which progenies in the following years were tested for productivity and other agronomic traits. Most of M_4 - M_5 mutants were discarded because of no breeding value. Mutated plants with higher or standard yield were chosen for the subsequent tests.

The estimation of selected mutant lines was done in the control, preliminary, and competitive strain tests in 1979-1984. These tests were carried out on the Dachnaya breeding station of All-Union Institute of Plant Breeding and Genetics. All these years, except for 1979 and 1984, were dry. 1983 was very dry; there were only 202 mm of rainfall. That is why soybean yield in dry land was very low. At the same time, the drought gave us a chance to choose a number of drought-resistant mutant forms.

In the control test nursery, plots were 4 m^2 with 2 replications, in preliminary and competitive strain tests with 4 and 6 replications, respectively. Nursery plots in the preliminary and competitive tests were 6 m^2 and

18 m², respectively. The nurseries were sown by SKS-6-10 drill. During the vegetation period, phenological tests and other observations were made. Plots were harvested by "Seedmaster" combine. Seed yield was calculated for 14% water content. Protein content was determined by Kjeldahl's method. Amino acid content, except for tryptophane and methionine, was studied by using amino acid analyzer KLA-5 (Hitachi, Japan). For this purpose, grain was milled by electromill and defatted by waterless chloroform. Protein hydrolyzation was made by 6M HCl at 110°C for 24 hr. Tryptophane content was determined in a separate flour sample by spectrofluorimetric method after protein hydrolyzation with papain. Methionine analysis was made by using nitroprussic reaction after enzymatic hydrolyzation by pronase. Amino acid content was designated as a percentage to fatless matter and to protein. NMU, NEU, and gamma-rays were the most effective in quantity of morphological mutations. EI had middle activity, EO, NDMU and DMS had practically the same activity, and induced 1-10% of mutations depending on variety and dose.

Studied mutagen factors induced such variations as earliness, lateness, lodging resistance, high production, tall-grown and stunted plants, dwarfness, color changes of pubescence and pods, increased and reduced number of pods per plant. It should be noted that early ripening mutants were often found. In our tests, dwarfs and tall-grown forms were found very seldom.

Yield evaluation at final stages of soybean breeding gave us an opportunity to find a number of promising soybean mutants. Some of these mutants out-yielded such commercial varieties in Odessa region as 'Bukuriya' and 'Belosnezshka'. Mutant M 1/4-80 was the most valuable. It was induced from variety VNIIMK 9186 by gaseous phase of DMS. During competitive varieties tests in 1980-1983, it out-yielded standard variety Bukuriya by 160 kg/ha. This mutant was characterized by higher protein content and short vegetation period. During 1980-1984, protein content exceeded the standard by 3.2%. This mutant was passed into the National Soybean Variety Trial under the name of 'Arkadiya Odesskaya'.

During the National Soybean Variety Trial, the new variety demonstrated good results in some regions of our republic. It out-yielded standard Bukuriya in these tests in Odessa region by 170 kg/ha. In that region, Arkadiya Odesskaya was characterized by higher productivity and protein content and also by early ripening, especially in the northern parts of the region. In 1983-1984, average vegetation period of Arkadiya Odesskaya in the Balta variety

test was 105 days, while Bukuriya had 118 days. On these grounds, Arkadiya Odesskaya is released in Odessa region beginning with 1986.

Yield structure analysis during several years showed that the new variety exceeded the standard variety by underground weight, number of nodes, pods and seeds per plant, seeds weight per plant and 1000-seed weight (Table 1). It also had higher harvest index, and bottom pods are higher, than those of the standard variety. Plants were not so tall-grown as the standard; that caused the increased lodging resistance.

It should be noted that Arkadiya Odesskaya is characterized by determinate growth type, that is a new trend in soybean breeding in our country. Determinate varieties are resistant to lodging, they can be sown by closed-drill method with increased seeding rate, so yield can be considerably higher due to more effective use of feeding area.

Arkadiya Odesskaya demonstrated great advantages with irrigation in Zaporozhshskaya region, where it out-yielded all studied forms (Table 2). Grain yield during the test period averaged 380 kg/ha higher than the standard variety. Arkadiya Odesskaya is considered prospective in this region since 1985.

In 1984, this variety was tested in seven regions of the Ukraine besides Odesskaya and Zaporozhshskaya regions. In some of these regions, it greatly out-yielded standard varieties. Nikolaevskaya region should be mentioned particularly because in both variety tests Arkadiya Odesskaya had the highest grain yield. In Voznesensky and Octjabrsky variety tests (Nikolaevskaya region) grain yield averaged 2280 kg/ha, while Bukuriya and Belosnezshka averaged 2040 kg/ha and 1860 kg/ha, respectively. These data and practice demonstrate that Arkadiya Odesskaya can yield 2500-2600 kg/ha in rainfed conditions and 3400-3500 kg/ha with irrigation.

It is of great importance that the new variety produces high yield both in rainfed conditions and with irrigation; that testifies to its good adaptability. The creation of this new variety gives us an opportunity to induce mutations with higher adaptability to environments.

The new variety is characterized by dense brown pubescence of plants and pods, purple color of hypocotyl and flowers. Plant height is average. Seeds are yellow, glossy with a well-marked longitudinal hilum.

Many agricultural crops show a significant decrease in protein quality associated with increase in protein content. Since Arkadiya Odesskaya is characterized by considerably increased protein content among other commercial

varieties, we tested total amino acid content of the studied variety in comparison with variety Bukuriya (Table 3). The data show that the increased protein content was not associated with decrease in total amino acid content. The studied variety and variety Bukuriya had no differences in such essential amino acids as lysin, tryptophane, histidine, threonine, valine, and methionine. The increased content of leucine, isoleucine, and phenylalanine is a positive characteristic of Arkadiya Odesskaya. Percentage of all essential amino acids in the variety was 16.87%, and that of Bukuriya was 16.38%.

Thus, the Arkadiya Odesskaya variety is characterized by high grain yield, increased protein content, and improved amino acid composition.

Since 1984, the new mutant variety Dachnanskaya I is in the National Soybean Variety Trial. In the competitive strain test in 1981-1984, it outyielded the standard variety by 360 kg/ha. That form was created by applying NEU in 0.0125% upon the seeds of VNIIMK 9186. The developed variety is characterized by increased resistance to some fungus disease, especially to fusarium blight of seedlings.

Now days, the group of mutants characterized by higher yield and improved agronomic characters is studied (Table 4). Apparently, some of them will be the ancestors of new varieties.

Table 1. Yield structure and some agronomic characters of soybean variety Arkadiya Odesskaya in comparison with Bukuriya

Trait	Arkadiya Odesskaya				Bukuriya			
	1981	1982	1984	Ave.	1981	1982	1984	Ave.
Plant weight, g	25.6	13.0	14.4	17.7	17.9	13.1	12.1	14.4
Plant height, cm	54.2	40.7	46.0	47.0	61.5	39.3	52.3	51.0
Height of 1st pod set, cm	11.3	12.1	9.3	10.9	9.4	10.3	10.1	9.9
Number of branches	4.6	4.6	3.5	4.2	3.1	4.7	3.7	3.8
Number of nodes	24.8	9.1	18.0	17.3	14.2	8.9	15.1	12.7
Number of pods	55.4	26.3	34.4	38.7	31.4	23.5	23.0	26.0
Number of seeds	89.6	44.1	54.1	62.6	62.8	44.6	38.1	48.5
Number of pods in a node	2.2	2.9	1.9	2.3	2.2	2.6	1.5	2.1
Number of seeds in a pod	1.6	1.7	1.6	1.6	2.0	1.9	1.7	1.9
Plant seeds weight, g	10.9	5.1	6.5	7.5	6.4	4.7	4.6	5.2
100-seed weight, g	12.2	11.6	12.0	11.9	10.2	10.5	12.1	10.9
Harvest index	0.43	0.39	0.45	0.42	0.36	0.36	0.38	0.37

Table 2. Grain yield of soybean varieties studied on Verchnechortitsky variety test (Zaporozhskaya region)

Variety	Grain yield, kg/ha		
	1983	1984	Average
Kirovogradskaya 4, standard	3000	2400	2700
Aurora	3080	2610	2840
Kirovogradskaya 26	3310	2380	2840
Arkadiya Odesskaya	3430	2720	3080

Table 3. Amino acids content of seeds of the variety Arkadiya Odesskaya

Amino acid	Amino acids content, %			
	In air-dry matter		In protein	
	Arkadiya	Bukuriya	Arkadiya	Bukuriya
Tryptophane	0.62	0.60	1.38	1.36
Lysine	2.94	2.98	6.52	6.74
Histidine	1.38	1.40	3.08	3.17
Arginine	3.24	3.28	7.19	7.42
Aspartic acid	5.79	5.80	12.35	13.14
Threonine	1.98	1.93	4.39	4.37
Serine	2.47	2.37	5.48	5.36
Glutamic acid	8.84	8.43	19.61	19.08
Proline	2.55	2.70	5.66	6.11
Glycine	1.96	1.97	4.35	4.46
Alanine	1.90	1.98	4.22	4.48
Valine	1.74	1.73	3.86	3.91
Methionine	0.54	0.52	1.20	1.18
Isoleucine	1.83	1.70	4.06	3.85
Leucine	3.50	3.37	7.77	7.63
Tyrosine	1.44	1.28	3.20	2.90
Phenylalanine	2.34	2.15	5.19	4.87

Table 4. Grain yield and some agronomic traits of promising soybean mutants

Mutant number	Initial variety	1984	Grain yield kg/ha	Grain content, %	
		Mutagenic factor		Protein	Lysine
—	Bukuriya, st	—	1340	32.8	1.98
34/82	Peremoga	gamma-rays	1760	34.8	1.76
16/82	Peremoga	gamma-rays	1780	34.0	1.86
18/82	Kirovogradskaya 4	NMU lg 10 days	1800	32.0	1.97
17/82	VNIIMK 9186	DMS 1ml 4 days	1930	33.2	2.36
29/82	Peremoga	EI 0.01%	1910	30.2	2.07
14/82	Hybrid 89-10	NMU 0.00625%	1890	35.8	2.20
42/82	Peremoga	gamma-rays	2030	33.6	2.24
28/82	Peremoga	NMU 0.0125%	1940	34.4	2.02
21/84	VNIIMK 9186	DMS 0.02%	1760	33.8	2.30
22/84	VNIIMK 9186	DMS 1ml 4 days	1980	33.6	1.86
23/84	Hybrid 115-92	gamma-rays	1920	35.0	2.07
26/84	Hybrid 115-92	gamma-rays	1930	31.6	2.23
27/84	Peremoga	EO 0.10%	1770	34.6	2.41
28/84	Peremoga	NDMU 0.0125%	1860	31.6	2.06
30/84	Kirovogradskaya 4	NMU 0.00625%	1790	33.6	2.16
31/84	Kirovogradskaya 4	DMS 0.01%	1840	32.4	2.25
33/84	Peremoga	DMS 0.02%	1800	35.0	2.62
48/84	Peremoga	gamma-rays	1800	33.4	2.24
49/84	VNIIMK 9186	DMS 1ml 2 days	1910	31.0	2.02
50/84	Peremoga	NDMU 0.0125%	1980	35.0	2.44
51/84	Peremoga	NDMU 0.0125%	2040	34.6	2.33
52/84	Peremoga	DMS 0.02%	2050	32.8	2.25

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1) Exotic soybean yield performance trial in the Mekong Delta in SR Vietnam.

The test was conducted on a brown, silty, clay loam. The soil was quite acid for soybeans, but it is fairly representative of the soil types in the area. With a pH of 5.1, there was an adequate amount of available calcium; however, the availability of N, P, and K was quite low.

Twelve varieties were included in the test. Ten of the varieties were products of plant breeding in the United States, one came from the Philippines, and one came from Brazil.

Germination was nearly 100% for all varieties in the test. Initial plant vigor was good. Overall plant development was adequate during the first three weeks of growth; however, several varieties began to flower within the fourth week after planting with a cessation of vegetative growth. Within six weeks after planting, all but 'Improved Pelican' and 'Santa Maria' were in full bloom or flowering had already peaked and pods were beginning to form. Further vegetative development had ceased by the sixth week in all but Improved Pelican, 'L 114', and Santa Maria.

Some explanation as to the dwarfness in this test can be attributed to the soybean plant's dependence upon the length of the dark period to initiate blooming. Soybean plants begin fruiting and mature primarily in response to changing daylengths, a condition referred to as photoperiod response. An exception was Improved Pelican, which performed independently of the photoperiod. During the dry season and at the beginning of the monsoon rains, temperatures are quite high and the daylength is much shorter than the optimum $14\frac{1}{2}$ hours required for most southern U.S. varieties. The daylength during this test ranged from approximately $12\frac{1}{2}$ to 13 hours, thus stimulating flowering soon after germination before the plants could significantly develop vegetatively.

Besides the dwarfed condition and early maturity noted in most varieties, other conditions such as the number of lateral branches, number of pods per plant and the number of seeds per pod might be of interest in determining adaptability.

It might be significant to note that 'Bragg', Maturity Group VII, even though the average plant height was only 23.25 cm, had almost double the number

of pods as any other variety in the test, including Santa Maria, Improved Pelican, or L 114. Bragg matured in less than 100 days, which is desirable, especially if soybeans are to be grown during the dry season away from a source of irrigation. 'Verdee', Maturity Group III, appeared to have been the variety most adversely affected by the photoperiod. Besides the dwarfed condition of the plant itself, the pods were small and wrinkled. Initially, the seed of Verdee were the largest planted. 'Hardee' appeared to have some possibility.

During the course of the test, plants were periodically pulled to examine the amount of nodulation. All varieties appeared to have sufficient nitrogen during growth except Improved Pelican. Upon examining the roots of this variety, no nodules were found, indicating that the strain of *Rhizobium* used is not specific for this variety. In all other varieties, the nodules observed were plentiful and pink on the interior indicating functional bacteria.

Another consideration that must be taken into account when growing short or dwarfed plants is competition from weeds when grown in the presently recommended row spacings. Even with the use of a herbicide that controlled weeds initially, the lack of shading by the soybean plants and heavy rainfall resulted in a serious weed problem that could only be corrected by hoeing or hand-pulling. Possibly by seeding initially in a narrower row, i.e., 25-30 cm, or by broadcasting seed of short or dwarfed varieties, the problem of weed competition can be overcome.

Soybean mosaic virus was observed in all varieties; however, it did not appear to have caused any serious problem. Very little damage was encountered by insects as the spray program with agricultural chemicals was effective.

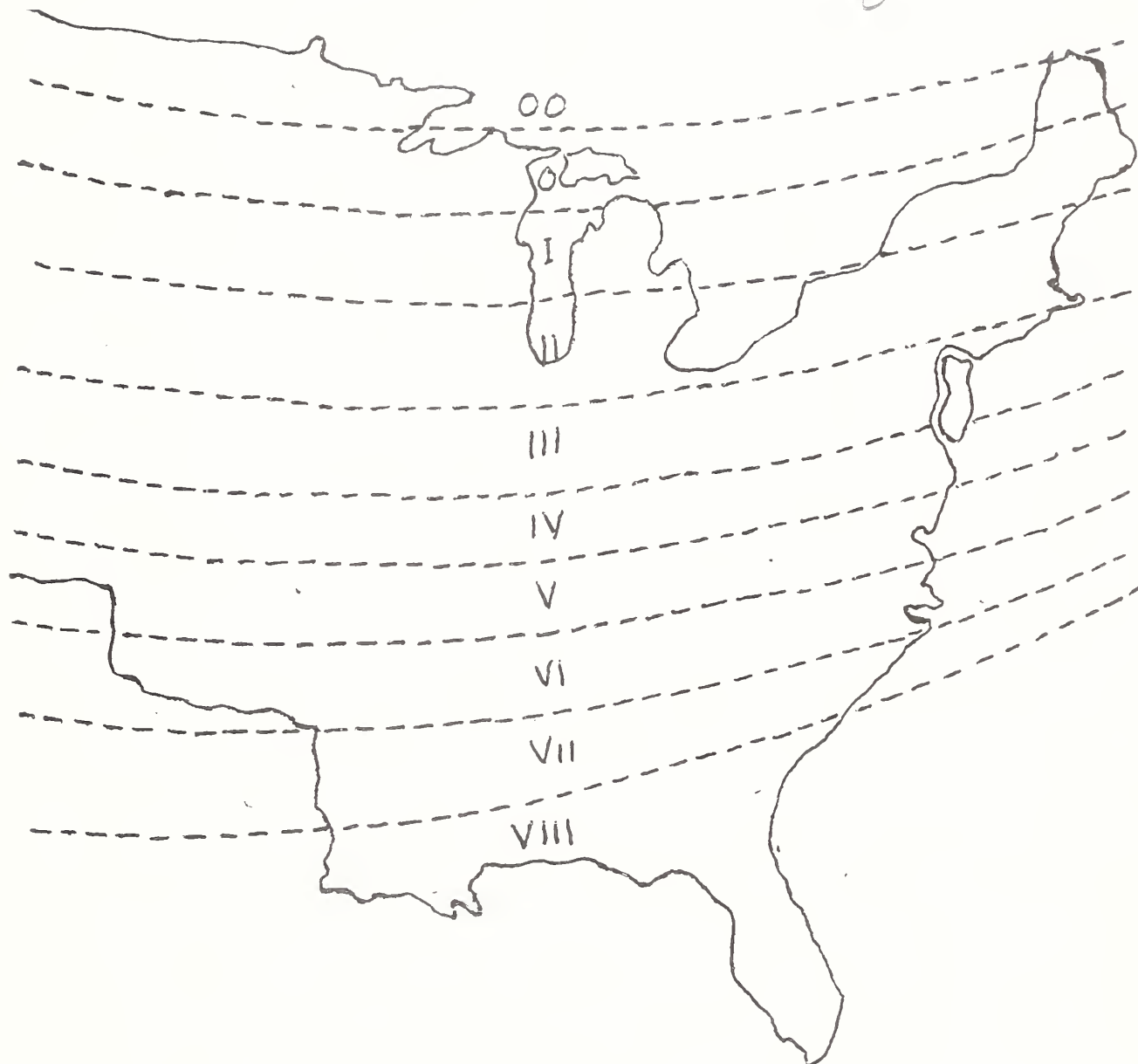
The test tended to confirm the suspicion that the majority of American varieties are generally not well-adapted to the Mekong Delta area of Vietnam. The main reason for this apparent lack of adaptability is the difference in photoperiod between the two areas. It is known that soybeans are extremely sensitive to changes in the photoperiod. Most U.S. varieties grown under Vietnam's photoperiod conditions will be early-maturing and dwarfed in size. In most cases, full season varieties generally yield more than those that mature very early.

Only varieties 'Bragg' and possibly Hardee of the dwarfed varieties appear to have any possibilities of eventual commercial production in Vietnam due to the heavy set of pods as well as their early maturity.

It is felt that Bragg and Hardee should also be tested further but on a narrower row to aid in weed control. By decreasing row width, there will be a need for a heavier rate of seeding; therefore, yields will have to be higher to justify the increased cost of seed.

If continued emphasis is placed on introducing and screening U.S. varieties, only those varieties that fall in Maturity Group VII and/or VIII should be considered.

Chu Huu Tin



There are 10 maturity classes of soybeans -- the higher the number, the later the maturity and the further south the variety is adapted for full-season use. The broken lines across the map are hypothetical. There are no clearly cut areas where variety is or is not adapted. (Adapted from *Modern Soybean Production* by W. O. Scott and S. R. Aldrich)

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Zambia

1) ²⁴⁷ Seed inoculation response for promiscuous soybean cultivars.

A major constraint in increasing soybean production in the developing countries is the availability of inoculum to small scale farmers in the remote areas of the country. This group of farmers also lack adequate storage facilities for the inoculum. This problem is being overcome by developing promiscuous soybean varieties in Zambia (Javaheri and Nyemba, 1982; Joshi et al., 1985) and at the International Institute of Tropical Agriculture, Ibadan, Nigeria (Kueneman et al., 1984). Soybean varieties that have the ability to form effective symbiotic relationships with a wide range of indigenous rhizobia are said to be promiscuous (Pulver et al., 1985).

The response of inoculants on promiscuous soybean varieties has not been fully investigated. Pulver et al. (1982) found several inoculants to be effective in increasing nodule mass on promiscuous varieties 'Orba', TGM 686, and 'Malanyan', but there was no significant increase in shoot dry weights at 60 days. It has also been observed that inoculation occasionally results in dark green plants and early vigorous growth in the season, but inoculation of promiscuous varieties does not always result in significant yield response (Kueneman et al., 1984; Joshi et al., 1985). The present investigation was undertaken to evaluate inoculant response of promiscuous soybean varieties over a long term period taking into account yearly changes in environmental factors such as drought or adequate rainfall.

Materials and methods. The experiment was planted on virgin land (sandy loam) on December 19, 1984, at the Magoye Regional Research Station, Magoye, Zambia. Magoye is situated at Latitude S, 16°00, Longitude E, 27°36', at an elevation of 1018 meters.

Sixteen promiscuous lines, including two recommended promiscuous cultivars, 'Magoye' and 'Hernon 147' and cultivar 'Kaleya' as nonpromiscuous check, were evaluated with and without inoculation, in a split plot design, cultivars being main plots and inoculum treatment as sub-plots. Each main plot consisted of 8 rows, 50 cm apart and 5 m long. Each sub-plot consisted of 4 rows. Yield data were recorded from one of the two central rows (50 cm x 4 m) of each sub-plot. In the two central rows, 50 cm at either end was treated as nonexperimental area. The other central row was used for nodule count.

Table 1. Yield of promiscuous soybean cultivars with and without seed inoculation

Cultivar	kg/ha	
	Without inoculation	With inoculation
1 P5	1894	1839
2 K39	1534	2114
3 K49-14	769	1530
4 Hernon 147	2301	2883
5 49-18	1168	2388
6 K8	723	1233
7 P7	1966	2508
8 K79	299	564
9 K152	1943	2291
10 K53	1818	1486
11 M27	2178	3682
12 M30	1828	766
13 K134	1692	2519
14 TGX326-034D	745	1372
15 TGX297-192C	1439	3002
16 Magoye	1925	2310
17 Kaleya	2025	3099
\bar{X}	1544	2093

Statistical analysis

C.V. (a) % = 31.36

C.V. (B) % = 21.26

S.E. \bar{x} (a) = ± 203.7 S.E. \bar{x} (b) = ± 47.36

	(a)	(b)
L.S.D. 5%	579.6	13.6
L.S.D. 1%	773.9	179.5
L.S.D. 0.1%	1012.4	234.5

Number of nodules/plant was recorded at 7 weeks after planting and at the end of flowering period for each treatment. Magoye Regional Research Station received 748.6 mm of rainfall during the 1984/85 season, whereas, during the 1983/84 season, rainfall at this site was only 588.6 mm.

Results and discussion. The overall mean yield without inoculum was 1544 kg/ha, and with inoculation 2093 kg/ha, a considerable increase of 35.6% over no inoculation (Table 1). During the 1983/84 growing season, yield increase with inoculation was only 3.2% for the same cultivars (Joshi et al., 1985). The high yield response to inoculation during the 1984/85 season can be attributed to adequate rainfall during the growing season (rainfall 1984/85 - 749 mm; 1983/84 - 589 mm). During the 1983/84 season, the overall mean yield without inoculation was 885 kg/ha and with inoculation 913 kg/ha.

The number of nodules/plant (Table 2), both at 7 weeks after planting and at the end of the flowering period, increased considerably with inoculation. The number of nodules/plant generally decreased at the end of the flowering period. Cultivar Kaleya (nonpromiscuous check) had the least number of nodules/plant at the end of 7 weeks and at the end of the flowering period without inoculation. Nodule dry weight/plant also was less with no inoculation than nodule dry weight/plant with inoculation both at 7 weeks after planting and at the end of the flowering period.

It appears that seed inoculation of promiscuous soybean cultivars increases seed yield under an adequate moisture regime, whereas it has very little effect on yield when the plants are under moisture stress.

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Table 2. Number of nodules/plant with and without seed inoculation

Cultivar	7 Weeks after planting		End of flowering	
	Without inoculum	With inoculum	Without inoculum	With inoculum
P5	18	44	12	24
K39	18	32	9	14
49-1	23	30	10	20
Hernon 147	6	35	6	23
49-18	29	39	19	20
K8	9	29	13	22
P7	15	31	8	23
K79	20	27	15	20
K152	15	32	10	17
K53	22	31	10	24
M27	20	33	9	14
M30	16	43	12	22
K4	10	34	10	20
TGX326-034D	4	30	7	23
TGX297-192C	4	40	8	27
Magoye	16	31	8	16
Kaleya	2	31	3	24
\bar{X}	15	34	10	21

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